

## SEARCH REQUEST FORM

Requestor's

Name:

Sally Teng

Serial

Number:

08/426,509

Date:

1/27/97

Phone:

308-4230

Art Unit:

1812

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search

- ① amino acids <sup>SH<sub>3</sub></sup> 48 to 111, <sup>Kinase</sup> 233-478, + <sup>SH<sub>2</sub></sup> 122-196  
of SEQ ID NO: 2
- ② amino acids 25 to 109, <sup>SH<sub>2</sub></sup> 296-375, <sup>SH<sub>3</sub></sup> 192-234,  
+ 424 to 659 <sup>Kinase</sup> of SEQ ID NO: 4
- ③ amino acids 122 to 201, 54 to 112, <sup>SH<sub>2</sub></sup> 247 to 426,  
of SEQ ID NO: 6
- ④ amino acids 493-507 of SEQ ID NO: 2
- ⑤ amino acids 666-675 of SEQ ID NO: 4

## STAFF USE ONLY

1-552

Date completed: 02-04-97

Searcher:

Beverly W. 8999

Terminal time:

15

Elapsed time:

CPU time:

Total time:

27

Number of Searches:

Number of Databases:

1

## Search Site

STIC

CM-1

Pre-S

## Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

## Vendors

IG

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other <sup>✓</sup> MIP



Title: >US-08-426-509-4  
Description: (192-234) from US08426509.pep (3 of 5)  
Perfect Score: 290  
Sequence: 1 AQYDNESKKNYGSQPPSSSTSLAQYDSNSKKIYGSQPNFNMQY 43

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 31.496; Variance 62.651; scale 0.503

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Query	Match	Length	DB	ID	Description	Pred. No.
1	80	27.6	473	14	S61428	late embryogenesis a	3.31e-01		
2	77	26.6	458	9	S33520	Lea protein - soybea	8.66e-01		
3	77	26.6	655	5	A55726	RNA-binding protein	8.66e-01		
4	77	26.6	656	5	A49358	RNA-binding protein	8.66e-01		
5	76	26.2	2710	8	A37052	toxin A - Clostridiu	1.19e+00		
6	76	26.2	2710	8	S08638	toxin A - Clostridiu	1.19e+00		
7	74	25.5	870	8	S27514	mosquitocidal toxin	2.22e+00		
8	72	24.8	462	13	S33798	FUS-CHOP mutant fusi	4.11e+00		
9	72	24.8	526	5	S33799	RNA-binding protein	4.11e+00		
10	70	24.1	286	9	S32480	hypothetical protein	7.52e+00		
11	70	24.1	1538	3	RGBYS3	regulatory protein S	7.52e+00		
12	70	24.1	1986	10	S28353	probable polyketide	7.52e+00		
13	69	23.8	173	8	S38231	hypothetical protein	1.01e+01		
14	69	23.8	774	3	QRECFA	iron(III) dicitrate	1.01e+01		
15	68	23.4	213	4	S26055	2-dehydro-3-deoxypho	1.36e+01		
16	68	23.4	328	4	S16300	UDPglucose 4-epinera	1.36e+01		
17	68	23.4	396	10	S58223	LSR1 protein - yeast	1.36e+01		
18	68	23.4	396	10	S61136	probable transcripti	1.36e+01		
19	68	23.4	573	12	S20710	hypothetical protein	1.36e+01		
20	68	23.4	1394	10	A29637	position-specific an	1.36e+01		
21	67	23.1	231	8	F64120	phosphate regulon tr	1.83e+01		
22	67	23.1	316	9	S58719	hypothetical protein	1.83e+01		
23	67	23.1	439	9	A36911	glutamine synthetase	1.83e+01		
24	67	23.1	664	10	S53037	PLB1 protein - yeast	1.83e+01		
25	67	23.1	889	10	S50934	hypothetical protein	1.83e+01		
26	67	23.1	1196	14	S35994	XP-G-related protein	1.83e+01		
27	66	22.8	288	6	I36848	ABR protein - variol	2.44e+01		
28	66	22.8	320	10	S09208	chorion protein s36	2.44e+01		
29	66	22.8	433	2	ITHUC	alpha-1-antichymotry	2.44e+01		
30	66	22.8	505	10	S44647	f42h10.1 protein - C	2.44e+01		
31	66	22.8	930	10	D37271	A-alpha 7 4 protein	2.44e+01		
32	66	22.8	1094	9	S49313	protein kinase - sli	2.44e+01		
33	66	22.8	1094	9	S52076	protein kinase - sli	2.44e+01		
34	66	22.8	1146	10	S46837	hypothetical protein	2.44e+01		
35	65	22.4	107	4	B60754	glucan 1,4-alpha-glu	3.25e+01		
36	65	22.4	131	7	JC1369	hypothetical 14.2K p	3.25e+01		

37	65	22.4	270	8	H64248	hypothetical protein	3.25e+01
38	65	22.4	657	4	A64079	2',3'-cyclic-nucleot	3.25e+01
39	65	22.4	1468	12	A44345	nucleoporin - rat	3.25e+01
40	64	22.1	125	10	S53086	ND3 protein - jelly	4.32e+01
41	64	22.1	295	13	S36174	RNA binding protein/	4.32e+01
42	64	22.1	330	14	J02262	Polygalacturonase in	4.32e+01
43	64	22.1	397	1	XNECY	tyrosine transaminas	4.32e+01
44	64	22.1	459	6	J02345	major capsid protein	4.32e+01
45	64	22.1	877	9	S58824	hypothetical protein	4.32e+01

# ALIGNMENTS

## RESULT 1

ENTRY S61428 #type complete  
 TITLE late embryogenesis abundant protein (clone pGPM10) - soybean  
 ORGANISM #formal\_name Glycine max #common\_name soybean  
 DATE 01-Mar-1996 #sequence\_revision 01-Mar-1996 #text\_change 01-Mar-1996  
 ACCESSIONS S61428  
 REFERENCE S61428  
 #authors Chow, T.; Hsing, Y.C.; Chen, Z.  
 #submission submitted to the EMBL Data Library, October 1993  
 #description cDNA sequences for a soybean seed maturation polypeptide gene family.  
 #accession S61428  
 ##status preliminary  
 ##residues 1-473 ##label CHO  
 ##cross-references EMBL:U02966  
 SUMMARY #length 473 #molecular-weight 50982 #checksum 278

Query Match 27.6%; Score 80; DB 14; Length 473;  
 Best Local Similarity 21.6%; Pred. No. 3.31e-01;  
 Matches 8; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Db 195 dyatqktkdyasdatdaakktkdyaqktkdyaseas 231  
 :| : |:|:|: :: :| : | |:|:|:  
 Qy 193 QYDNESKKNYGSQPPSSSTSLAQYDSNSKKIYGSQPN 229

## RESULT 2

ENTRY S33520 #type complete  
 TITLE Lea protein - soybean  
 ORGANISM #formal\_name Glycine max #common\_name soybean  
 DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
 ACCESSIONS S33520  
 REFERENCE S33520  
 #authors Chow, T.; Hsing, Y.C.; Chen, Z.  
 #submission submitted to the EMBL Data Library, June 1993  
 #description cDNA sequences for a soybean seed maturation polypeptide gene family.  
 #accession S33520  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-458 ##label CHO  
 ##cross-references EMBL:Z22872  
 SUMMARY #length 458 #molecular-weight 49399 #checksum 5605

Query Match 26.6%; Score 77; DB 9; Length 458;  
 Best Local Similarity 22.2%; Pred. No. 8.66e-01;  
 Matches 8; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Db 181 dyatqktkdyasdatdaakktkdyaqktkdyasda 216  
 :| : |:|:|: :: :| : | |:|:|:  
 Qy 193 QYDNESKKNYGSQPPSSSTSLAQYDSNSKKIYGSQPN 228

Search completed: Mon Feb 3 17:00:21 1997

Job time : 10 secs.

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MASPAR (TM)

\*\*\*\*\*

Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:59:28 1997; MasPar time 4.51 Seconds  
456.034 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-4  
Description: (296-375) from US08426509.pep (2 of 5)  
Perfect Score: 579  
Sequence: 1 WFAGNISRSQSEQLLRQKGK.....ENKLYLAENYCFDSIPKLIH 80

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 37.725; Variance 82.158; scale 0.459

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Match	Query Length	DB ID	Description	Pred. No.
1	325	56.1	659	11	I37212	Bruton agammaglobuli	8.36e-39
2	325	56.1	659	11	S28912	protein-tyrosine kin	8.36e-39
3	324	56.0	659	12	B45184	B cell progenitor ki	1.26e-38
4	324	56.0	660	12	JN0471	protein-tyrosine kin	1.26e-38
5	319	55.1	442	11	A45184	B cell progenitor ki	9.71e-38
6	311	53.7	620	4	S33253	protein-tyrosine kin	2.54e-36
7	307	53.0	619	4	JN0472	protein-tyrosine kin	1.29e-35
8	307	53.0	619	4	A47333	T-cell-specific tyro	1.29e-35
9	307	53.0	625	4	A43030	protein-tyrosine kin	1.29e-35
10	300	51.8	527	12	A55631	protein-tyrosine kin	2.21e-34

11	291	50.3	527	4	S13763	protein-tyrosine kin	8.42e-33
12	291	50.3	602	4	JU0215	tyrosine kinase, tec	8.42e-33
13	291	50.3	608	4	JU0227	protein-tyrosine kin	8.42e-33
14	291	50.3	630	4	JU0228	protein tyrosine kin	8.42e-33
15	254	43.9	590	1	TVFFDS	protein-tyrosine kin	2.23e-26
16	166	28.7	499	4	A40092	protein-tyrosine kin	8.32e-12
17	166	28.7	505	1	TVHUHC	protein-tyrosine kin	8.32e-12
18	162	28.0	517	4	A43807	protein-tyrosine kin	3.53e-11
19	161	27.8	537	4	A45501	protein-tyrosine kin	5.05e-11
20	160	27.6	517	12	S24547	protein-tyrosine kin	7.24e-11
21	159	27.5	503	4	J01321	protein-tyrosine kin	1.04e-10
22	159	27.5	503	1	TVMSHC	protein-tyrosine kin	1.04e-10
23	158	27.3	528	1	TVFVG9	protein-tyrosine kin	1.48e-10
24	158	27.3	541	1	TVCHYS	protein-tyrosine kin	1.48e-10
25	158	27.3	543	1	TVHUYS	protein-tyrosine kin	1.48e-10
26	158	27.3	557	10	A00629	protein-tyrosine kin	1.48e-10
27	157	27.1	541	4	A43610	protein-tyrosine kin	2.12e-10
28	157	27.1	541	12	S31645	protein-tyrosine kin	2.12e-10
29	157	27.1	542	1	TVHUSC	protein-tyrosine kin	2.12e-10
30	156	26.9	529	1	TVHUFR	protein-tyrosine kin	3.03e-10
31	155	26.8	526	1	TVFV60	protein-tyrosine kin	4.32e-10
32	155	26.8	533	1	TVCHS	protein-tyrosine kin	4.32e-10
33	155	26.8	539	11	B49114	protein-tyrosine kin	4.32e-10
34	155	26.8	557	1	TVFVS2	protein-tyrosine kin	4.32e-10
35	155	26.8	587	1	TVFVPR	protein-tyrosine kin	4.32e-10
36	154	26.6	663	1	TMVRR	protein-tyrosine kin	6.16e-10
37	154	26.6	1290	11	A36466	1-phosphatidylinosit	6.16e-10
38	154	26.6	1290	12	A31317	1-phosphatidylinosit	6.16e-10
39	154	26.6	1291	12	S00666	1-phosphatidylinosit	6.16e-10
40	153	26.4	536	4	S33569	protein-tyrosine kin	8.79e-10
41	153	26.4	981	1	F0HVGM	gag-abl polyprotein	8.79e-10
42	153	26.4	1123	4	A39962	kinase-related trans	8.79e-10
43	153	26.4	1130	1	TVHUA	protein-tyrosine kin	8.79e-10
44	152	26.3	526	1	TVFVR	protein-tyrosine kin	1.25e-09
45	152	26.3	568	1	TVFVS1	protein-tyrosine kin	1.25e-09

# ALIGNMENTS

```

RESULT      1
ENTRY       I37212      #type complete
TITLE       Bruton agammaglobulinemia tyrosine kinase - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change
              09-Mar-1996
ACCESSIONS  I37212
REFERENCE   I37212
#authors    Ohta, Y.; Haire, R.N.; Litman, R.T.; Fu, S.M.; Nelson, R.P.;
              Kratz, J.; Kornfeld, S.J.; de la Morena, M.; Good, R.A.;
              Litman, G.W.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9062-9066
#title       Genomic organization and structure of Bruton
              agammaglobulinemia tyrosine kinase: localization of
              mutations associated with varied clinical presentations and
              course in X chromosome-linked agammaglobulinemia.
#cross-references NUID:94377492
#accession   I37212
##status     preliminary
##molecule_type DNA
##residues    1-659 ##label RES
##cross-references EMBL:U10087; NID:g517436; CDS_PID:g517438
##note        only intron-exon junctions are shown

GENETICS
#gene        GDB:BTK; AGMX1; IND1
##cross-references GDB:G00-120-542
#map position Xq21.33-q22

```

#introns 47/3; 80/3; 103/3; 131/1; 174/1; 196/3; 259/2; 280/2; 298/3;

325/2; 368/1; 393/1; 450/2; 522/3; 544/2; 584/1; 636/3

SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 56.1%; Score 325; DB 11; Length 659;  
Best Local Similarity 48.8%; Pred. No. 8.36e-39;  
Matches 39; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhntsrqaeqlkqegkeggfivrdsskagkytvsfvakstgdpqgvirhyvvcstp 340  
|:: ::|||:||||:| ||||:|:|:| | :|||:|:|: | | :|| | : :

Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsyyylaekhlfstipelin 360  
:: |||: | :| |:

Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 2

ENTRY S28912 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) atk - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 25-Feb-1994 #sequence\_revision 01-Sep-1995 #text\_change  
01-Dec-1995

ACCESSIONS S28912

REFERENCE S28912

#authors Vetrie, D.; Vorechovsky, I.; Sideras, P.; Holland, J.;  
Davies, A.; Flinter, F.; Hammarstroem, L.; Kinnon, C.;  
Levinsky, R.; Bobrow, M.; Smith, C.I.E.; Bentley, D.R.

#journal Nature (1993) 361:226-233

#title The gene involved in X-linked agammaglobulinaemia is a member  
of the src family of protein-tyrosine kinases.

#accession S28912

##status preliminary

##molecule\_type mRNA

##residues 1-659 ##label VET

CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2  
homology

KEYWORDS phosphotransferase

FEATURE

221-269 #domain SH3 homology #label SH3\

281-377 #domain SH2 homology #label SH2\

400-658 #domain protein kinase homology #label KIN

SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 56.1%; Score 325; DB 11; Length 659;  
Best Local Similarity 48.8%; Pred. No. 8.36e-39;  
Matches 39; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhntsrqaeqlkqegkeggfivrdsskagkytvsfvakstgdpqgvirhyvvcstp 340  
|:: ::|||:||||:| ||||:|:|:| | :|||:|:|: | | :|| | : :

Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsyyylaekhlfstipelin 360  
:: |||: | :| |:

Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 3

ENTRY B45184 #type complete

TITLE B cell progenitor kinase, BPK=cytoplasmic tyrosine kinase -  
mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change  
12-May-1995

ACCESSIONS B45184

REFERENCE A45184

#authors Tsukada, S.; Saffran, D.C.; Rawlings, D.J.; Parolini, O.;  
 Allen, R.C.; Klisak, I.; Sparkes, R.S.; Kubagawa, H.;  
 Mohandas, T.; Quan, S.; Belmont, J.W.; Cooper, M.D.;  
 Conley, M.E.; Witte, O.N.

#journal Cell (1993) 72:279-290

#title Deficient expression of a B cell cytoplasmic tyrosine kinase  
 in human X-linked agammaglobulinemia.

#cross-references MUID:93145329

#accession B45184

##status preliminary; not compared with conceptual translation

##molecule\_type nucleic acid

##residues 1-659 ##label TSU

##cross-references NCBIP:123834

##experimental\_source 70z/3 pre-B cell line1

##note sequence extracted from NCBI backbone

CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2  
 homology

FEATURE

221-269 #domain SH3 homology #label SH3\  
 281-377 #domain SH2 homology #label SH2\  
 400-658 #domain protein kinase homology #label KIN

SUMMARY #length 659 #molecular-weight 76326 #checksum 9917

Query Match 56.0%; Score 324; DB 12; Length 659;  
 Best Local Similarity 47.5%; Pred. No. 1.26e-38;  
 Matches 38; Conservative 24; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhmtrsqaeqlkqegkeggfivrdsskagkytvsvfakstgepggvirhyvvcstp 340  
 |:: ::|||:||||:| |||:|:|:| |::|||:|:|: : |::|| |::|  
 Qy 296 WFAGNISRSQSEQLLRQKKEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355

Db 341 qsqqylaekhlfstipelin 360  
 :: |||: |::| ||:  
 Qy 356 ENKLYLAENYCFDSIPKLIH 375

#### RESULT 4

ENTRY JN0471 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) emb - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change  
 12-May-1995

ACCESSIONS JN0471

REFERENCE JN0471

#authors Yamada, N.; Kawakami, Y.; Kimura, H.; Fukamachi, H.; Baier,  
 G.; Altman, A.; Kato, T.; Inagaki, Y.; Kawakami, T.

#journal Biochem. Biophys. Res. Commun. (1993) 192:231-240

#title Structure and expression of novel protein-tyrosine kinases,  
 Emb and Ent, in the hematopoietic cells.

#accession JN0471

##molecule\_type mRNA

##residues 1-660 ##label YAM

##note the nucleotide sequence is not given

GENETICS

#gene emb

CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2  
 homology

KEYWORDS phosphotransferase

FEATURE

223-271 #domain SH3 homology #label SH3\  
 283-379 #domain SH2 homology #label SH2\  
 402-659 #domain protein kinase homology #label KIN\  
 552 #binding\_site phosphate (Tyr) (covalent) #status  
 predicted

SUMMARY #length 660 #molecular-weight 76577 #checksum 1680

Query Match 56.0%; Score 324; DB 12; Length 660;  
Best Local Similarity 47.5%; Pred. No. 1.26e-38;  
Matches 38; Conservative 24; Mismatches 18; Indels 0; Gaps 0;

Db 283 wyskhntsrqaeqlkqegkeggfivrdsskagkytvsvfakstgepqgvirhyvvcstp 342  
|:: ::|||:||||:| ||||:|:|:| | :|||:|:|: : | ::|| | : :  
Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355  
  
Db 343 qsyyylaekhlfstipelin 362  
:: |||: | :| | :|  
Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 5

ENTRY A45184 #type fragment  
TITLE B cell progenitor kinase - human (fragment)  
CONTAINS tyrosine kinase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change  
19-Oct-1995  
ACCESSIONS A45184  
REFERENCE A45184  
#authors Tsukada, S.; Saffran, D.C.; Rawlings, D.J.; Parolini, O.;  
Allen, R.C.; Klisak, I.; Sparkes, R.S.; Kubagawa, H.;  
Mohandas, T.; Guan, S.; Belmont, J.W.; Cooper, M.D.;  
Conley, M.E.; Witte, O.N.  
#journal Cell (1993) 72:279-290  
#title Deficient expression of a B cell cytoplasmic tyrosine kinase  
in human X-linked agammaglobulinemia.  
#cross-references MUID:93145329  
#accession A45184  
##status preliminary; not compared with conceptual translation  
##molecule\_type nucleic acid  
##residues 1-442 ##label TSU  
##cross-references NCBIP:123835  
##experimental\_source erythroleukemia cell line K562  
##note sequence extracted from NCBI backbone  
CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2  
homology  
FEATURE  
221-269 #domain SH3 homology #label SH3\  
281-377 #domain SH2 homology #label SH2\  
400-442 #domain protein kinase homology (fragment) #label KIN  
SUMMARY #length 442 #checksum 2964

Query Match 55.1%; Score 319; DB 11; Length 442;  
Best Local Similarity 47.5%; Pred. No. 9.71e-38;  
Matches 38; Conservative 24; Mismatches 18; Indels 0; Gaps 0;

Db 281 wyskhntsrqaeqlkqegkeggfivrdsskaakytvsvfakstgdpqgvirhyvvcstp 340  
|:: ::|||:||||:| ||||:|:|:| | :|||:|:|: | | :|| | : :  
Qy 296 WFAGNISRSQSEQLLRQKGKEGAFMVRNSSQVGMVTVSLFSKAVNDKKGTVKHYHVHTNA 355  
  
Db 341 qsyyylaekhlfstipelin 360  
:: |||: | :| | :|  
Qy 356 ENKLYLAENYCFDSIPKLIH 375

RESULT 6

ENTRY S33253 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 02-Dec-1993 #sequence\_revision 01-Sep-1995 #text\_change  
19-Oct-1995  
ACCESSIONS S33253  
REFERENCE S33253

CC transformation. Such compounds have value in the treatment of  
CC chronic, acute myelogenous or acute lymphocytic leukaemia.  
SQ Sequence 1336 AA;

Query Match 7.7%; Score 85; DB 15; Length 1336;  
Best Local Similarity 27.3%; Pred. No. 9.62e+00;  
Matches 12; Conservative 15; Mismatches 15; Indels 2; Gaps 2;

Db 515 kvqindkddtseykhafeiilkdgnsvifsaksaeknnuuaal 558  
|| :: : | :|:| || :::: | : | ||  
Qy 65 KVNLEE-QTPVERQYPFQIVYKDGLLYVYASN-EESRSQWLKAL 106

Search completed: Mon Feb 3 16:54:34 1997  
Job time : 30 secs.

\*\*\*\*\*

MASSAL (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 16:52:39 1997; MasPar time 6.14 Seconds  
607.923 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-4  
Description: (25-169) from US08426509.pep (1 of 5)  
Perfect Score: 1102  
Sequence: 1 NYKERLFVLTKTNLSVYEYD.....ANLHTAVNEEKHRVPTFPDR 145

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 41.009; Variance 85.671; scale 0.479

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
--------	-----	-------	-------	--------	----	----	-------------	-----------

1	447	40.6	602	4	JU0215	tyrosine kinase, tec	6.81e-62
2	447	40.6	608	4	JU0227	protein-tyrosine kin	6.81e-62
3	447	40.6	630	4	JU0228	protein tyrosine kin	6.81e-62
4	423	38.4	620	4	S33253	protein-tyrosine kin	2.39e-57
5	413	37.5	619	4	JN0472	protein-tyrosine kin	1.84e-55
6	413	37.5	619	4	A47333	T-cell-specific tyro	1.84e-55
7	368	33.4	625	4	A43030	protein-tyrosine kin	4.92e-47
8	314	28.5	442	11	A45184	B cell progenitor ki	4.39e-37
9	314	28.5	659	11	S28912	protein-tyrosine kin	4.39e-37
10	314	28.5	659	11	I37212	Bruton agammaglobuli	4.39e-37
11	314	28.5	660	12	JN0471	protein-tyrosine kin	4.39e-37
12	313	28.4	659	12	B45184	B cell progenitor ki	6.68e-37
13	225	20.4	847	12	A56039	GTPase-activating pr	2.97e-21
14	202	18.3	527	4	S13763	protein-tyrosine kin	2.46e-17
15	142	12.9	1165	11	A42142	gap1 protein - fruit	1.14e-07
16	142	12.9	1165	10	S27809	GTPase-activating pr	1.14e-07
17	116	10.5	205	7	JU0223	hypothetical 24K pro	7.29e-04
18	98	8.9	350	11	S00755	pleckstrin - human	1.90e-01
19	97	8.8	1042	4	A33881	Ca2+-transporting AT	2.55e-01
20	97	8.8	1042	1	PWRBMC	Ca2+-transporting AT	2.55e-01
21	92	8.3	218	9	S47016	hypothetical protein	1.08e+00
22	91	8.3	348	4	JN0633	caricain (EC 3.4.22.	1.43e+00
23	91	8.3	454	7	B64107	chromosomal replicat	1.43e+00
24	90	8.2	345	1	PPPA	papain (EC 3.4.22.2)	1.89e+00
25	90	8.2	2223	11	A47447	calcium channel prot	1.89e+00
26	88	8.0	549	9	S46029	hypothetical protein	3.29e+00
27	88	8.0	1928	12	JS0610	beta-galactosidase (	3.29e+00
28	87	7.9	328	9	S45998	hypothetical protein	4.33e+00
29	86	7.8	458	10	S57605	hypothetical protein	5.68e+00
30	86	7.8	704	14	S61612	hypothetical protein	5.68e+00
31	86	7.8	775	9	S35543	DNA-directed DNA pol	5.68e+00
32	86	7.8	1549	2	A40691	trichohyalin - sheep	5.68e+00
33	85	7.7	97	7	B37141	parC protein - Esche	7.43e+00
34	85	7.7	104	7	B47062	pyocin positive regu	7.43e+00
35	85	7.7	362	12	A38135	ADP-ribosylarginine	7.43e+00
36	85	7.7	807	11	A34581	oxysterol-binding pr	7.43e+00
37	85	7.7	809	12	A34404	oxysterol-binding pr	7.43e+00
38	85	7.7	1336	12	S25716	SOS-1 protein - mous	7.43e+00
39	85	7.7	1487	4	S15904	alpha-1 proteinase i	7.43e+00
40	84	7.6	329	8	H64143	hypothetical protein	9.71e+00
41	83	7.5	305	8	S47261	cheR protein - Rhodo	1.26e+01
42	83	7.5	2009	10	A31068	SEC7 protein - yeast	1.26e+01
43	82	7.4	813	11	B47485	ABR protein 2 - huma	1.64e+01
44	82	7.4	822	11	A47485	ABR protein 1 - huma	1.64e+01
45	82	7.4	1477	4	A29952	alpha-1-inhibitor II	1.64e+01

# ALIGNMENTS

```

RESULT      1
ENTRY       JU0215      #type complete
TITLE       tyrosine kinase, tec type II - mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
            01-Dec-1995
ACCESSIONS  JU0215
REFERENCE   JU0215
#authors    Mano, H.; Mano, K.; Copeland, N.; Ihle, J.N.
#submission submitted to JIPID, December 1991
#accession  JU0215
##molecule_type mRNA
##residues   1-602 ##label MAN
##experimental_source liver, strain Balb/c
GENETICS
#gene       tec

```

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase  
homology; SH2 homology; SH3 homology  
KEYWORDS kinase-related transforming protein  
FEATURE  
185-223 #domain SH3 homology #status atypical #label SH3\  
345-602 #domain protein kinase homology #label KIN\  
353-361 #region protein kinase ATP-binding motif\  
496 #binding\_site phosphate (Tyr) (covalent) (by  
autophosphorylation) #status predicted  
SUMMARY #length 602 #molecular-weight 70103 #checksum 7992  
  
Query Match 40.6%; Score 447; DB 4; Length 602;  
Best Local Similarity 45.8%; Pred. No. 6.81e-62;  
Matches 55; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

Db 25 nykerlcvlpksvlsyye-graekkyrkavidiskikcveivknddgvipcqnfqpfqv 83  
||||| || | : ||||| : : ||| | : ||: ||| | : : | : : ||| :  
Qy 25 NYKERLFVLTKNLSYYEYDKMKRGSRKGSIEIKKIRCVEKNLEEQT-PVERQYPFQIV 83  
  
Db 84 hdantlyifapspqsrdruvkkkleeiknnnninikyhpkwadgsyqccrqtclapgc 143  
||: ||: : || : ||: | ||: | : ||: ||| : | || : ||: | : ||||  
Qy 84 YKDGLLYVYASNEESRSQWLKALQKEIRGNPHLLVKYHSGFFVDGKFLCCQGSCKAAPGC 143

# RESULT 2

ENTRY JU0227 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) tec III - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change  
01-Dec-1995  
ACCESSIONS JU0227  
REFERENCE JU0227  
#authors Mano, H.; Sato, K.; Yazaki, Y.; Hirai, H.  
#submission submitted to JIPID, March 1993  
#description The Tec protein-tyrosine kinase is involved in the IL-3  
signaling pathway in a murine myeloid cell line.  
#accession JU0227  
##molecule\_type mRNA  
##residues 1-608 ##label MAN  
GENETICS  
#gene Tec  
CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase  
homology; SH2 homology; SH3 homology  
KEYWORDS kinase-related transforming protein; phosphotransferase  
FEATURE  
185-223 #domain SH3 homology #status atypical #label SH3\  
345-603 #domain protein kinase homology #label KIN\  
496 #binding\_site phosphate (Tyr) (covalent) #status  
predicted  
SUMMARY #length 608 #molecular-weight 71162 #checksum 1974  
  
Query Match 40.6%; Score 447; DB 4; Length 608;  
Best Local Similarity 45.8%; Pred. No. 6.81e-62;  
Matches 55; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

Db 25 nykerlcvlpksvlsyye-graekkyrkavidiskikcveivknddgvipcqnfqpfqv 83  
||||| || | : ||||| : : ||| | : ||: ||| | : : | : : ||| :  
Qy 25 NYKERLFVLTKNLSYYEYDKMKRGSRKGSIEIKKIRCVEKNLEEQT-PVERQYPFQIV 83  
  
Db 84 hdantlyifapspqsrdruvkkkleeiknnnninikyhpkwadgsyqccrqtclapgc 143  
||: ||: : || : ||: | ||: | : ||: ||| : | || : ||: | : ||||  
Qy 84 YKDGLLYVYASNEESRSQWLKALQKEIRGNPHLLVKYHSGFFVDGKFLCCQGSCKAAPGC 143

# RESULT 3

ENTRY JU0228 #type complete

TITLE protein tyrosine kinase (EC 2.7.1.-) tec IV - mouse  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change  
 21-Mar-1996  
 ACCESSIONS JU0228  
 REFERENCE JU0228  
 #authors Mano, H.; Sato, K.; Yazaki, Y.; Hirai, H.  
 #submission submitted to JIPID, April 1993  
 #accession JU0228  
 ##molecule\_type DNA  
 ##residues 1-630 ##label MAN  
 ##experimental\_source myeloid  
 CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase  
 homology; SH2 homology; SH3 homology  
 KEYWORDS kinase-related transforming protein; phosphotransferase  
 FEATURE  
 185-233 #domain SH3 homology #label SH3\  
 246-344 #domain SH2 homology #label SH2\  
 367-625 #domain protein kinase homology #label KIN\  
 375-383 #region protein kinase ATP-binding motif\  
 515 #active\_site Asp (aspartylphosphate intermediate)  
 #status predicted  
 SUMMARY #length 630 #molecular-weight 73651 #checksum 4354


Query Match 40.6%; Score 447; DB 4; Length 630;  
 Best Local Similarity 45.8%; Pred. No. 6.81e-62;  
 Matches 55; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

Db 25 nykerlcvlpksvlsyye-graekkyrkvidiskikcveivknddgvipcqnfqfvv 83  
 ||||| || | : |||| : : ||| | : |||| : : | : :|||  
 Qy 25 NYKERLFVLTKTNLSYYEYDKMKRGSRKGSIEIKKIRCVEKNLEEGT-PVERQYPFQIV 83  
 Db 84 hdantlyifapspqsrdrwvkkkleeiknnnnimikyhpkwadgsyqccrqlapgc 143  
 ||::|| : || :|| | || | ::||| : || : ||| : ||||  
 Qy 84 YKDGLLYVYASNEESRSQWLKALQKEIRGNPHLLVKYHSGFFVDGKFLCCQSQCKAAPGC 143

RESULT 4  
 ENTRY S33253 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 02-Dec-1993 #sequence\_revision 01-Sep-1995 #text\_change  
 19-Oct-1995  
 ACCESSIONS S33253  
 REFERENCE S33253  
 #authors Tanaka, N.; Asao, H.; Ohtani, K.; Nakanura, M.; Sugamura, K.  
 #journal FEBS Lett. (1993) 324:1-5  
 #title A novel human tyrosine kinase gene inducible in T cells by  
 interleukin 2.  
 #accession S33253  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-620 ##label TAN  
 ##cross-references EMBL:D13720  
 CLASSIFICATION #superfamily SH3 homology; protein kinase homology  
 KEYWORDS phosphotransferase  
 FEATURE  
 178-226 #domain SH3 homology #label SH3\  
 361-619 #domain protein kinase homology #label KIN  
 SUMMARY #length 620 #molecular-weight 71830 #checksum 8123

Query Match 38.4%; Score 423; DB 4; Length 620;  
 Best Local Similarity 46.0%; Pred. No. 2.39e-57;  
 Matches 57; Conservative 26; Mismatches 41; Indels 0; Gaps 0;

Db 25 nfkvrffvltkaslaufedrghqkrtlkqsielsrikcveivksdisipchukupfvvh 84



(TM)

[illegible]

**MPsrch\_pp** protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated.

```
Title:                >US-08-426-509-2
Description:          (493-507) from US08426509.pep (4 of 4)
Perfect Score:       92
Sequence:             1 GQDADGSTSPRSQEP 15
```

Scoring table: PAM 150  
Gap 11

**Searched:** 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

```
Database: pir48
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
14:unrev
```

Statistics: Mean 22.865; Variance 34.220; scale 0.668

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	%		Length	DB	ID	Description	Pred. No.
	Score	Query Match					
1	92	100.0	507	4	A55625	protein-tyrosine kin	4.02e-08
2	75	81.5	465	4	B55625	protein-tyrosine kin	1.99e-04
3	75	81.5	465	12	I48926	protein-tyrosine kin	1.99e-04
4	54	58.7	156	3	Q0BEG9	HHRF1 protein - huma	2.65e+00
5	54	58.7	755	12	S32103	filensin - bovine	2.65e+00
6	52	56.5	717	6	S31034	retrovirus-related g	6.01e+00
7	52	56.5	717	6	S31035	retrovirus-related g	6.01e+00
8	51	55.4	1004	9	JC2221	major surface glycop	8.99e+00
9	50	54.3	41	11	A47602	complement C3b/C4b r	1.34e+01
10	50	54.3	195	11	S31861	myristylated alanine	1.34e+01
11	50	54.3	200	12	S17185	myristoylated alanin	1.34e+01
12	50	54.3	226	12	A26964	neuronal growth-rela	1.34e+01
13	50	54.3	227	12	A29800	neuromodulin - mouse	1.34e+01

14	50	54.3	545	7	F64181	CTP synthetase (pyrG	1.34e+01
15	50	54.3	2039	11	S03843	complement C3b/C4b r	1.34e+01
16	49	53.3	133	5	S24315	motilin precursor -	1.98e+01
17	49	53.3	351	12	A56387	helix-loop-helix tra	1.98e+01
18	49	53.3	436	7	S13583	nosD protein precurs	1.98e+01
19	49	53.3	471	7	S35635	DNA injection protei	1.98e+01
20	49	53.3	590	12	A40437	glutamic acid-rich p	1.98e+01
21	49	53.3	926	12	A54142	nucleoporin NUP107 -	1.98e+01
22	48	52.2	188	10	S44817	F44E2.2 protein - Ca	2.92e+01
23	48	52.2	559	11	B56731	chromatin assembly f	2.92e+01
24	48	52.2	627	10	A44112	spidroin 2, dragline	2.92e+01
25	48	52.2	1101	8	S15271	endoglucanase cenC -	2.92e+01
26	48	52.2	1396	12	A44453	translation initiati	2.92e+01
27	48	52.2	3566	11	A40701	tenascin-X precursor	2.92e+01
28	47	51.1	179	12	JH0499	glutamine/glutamic a	4.28e+01
29	47	51.1	189	14	D49600	genome-linked protei	4.28e+01
30	47	51.1	190	2	RHSHCE	corticoliberin precu	4.28e+01
31	47	51.1	315	6	D48560	immediate-early prot	4.28e+01
32	47	51.1	332	10	S60935	Lpe17 protein - yeas	4.28e+01
33	47	51.1	357	6	S18236	omega secalin precur	4.28e+01
34	47	51.1	357	6	S18235	omega secalin precur	4.28e+01
35	47	51.1	401	14	S58355	CP49 protein - chick	4.28e+01
36	47	51.1	425	5	A26431	nerve growth factor	4.28e+01
37	47	51.1	427	2	GQHUN	nerve growth factor	4.28e+01
38	47	51.1	450	11	S58351	CP49ins protein - ch	4.28e+01
39	47	51.1	479	11	A34924	complement C3b/C4b r	4.28e+01
40	47	51.1	591	11	A45135	profilaggrin - human	4.28e+01
41	47	51.1	664	2	VEHULA	lamin A - human	4.28e+01
42	47	51.1	713	11	S42803	fibroblast growth fa	4.28e+01
43	47	51.1	775	3	EDBE11	immediate-early prot	4.28e+01
44	47	51.1	1772	10	A45532	major merozoite surf	4.28e+01
45	47	51.1	2248	11	A35938	profilaggrin - human	4.28e+01

# ALIGNMENTS

RESULT 1

ENTRY A55625 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112),  
megakaryocyte-associated - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change  
01-Mar-1996

ACCESSIONS A55625; S43533

REFERENCE A55625

#authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,  
L.L.; White, R.A.; Avraham, H.

#journal J. Biol. Chem. (1995) 270:1833-1842

#title Structural and functional studies of the intracellular  
tyrosine kinase MATK gene and its translated product.

#accession A55625

##status preliminary; not compared with conceptual translation

##molecule\_type DNA

##residues 1-507 ##label AVR

REFERENCE S43533

#authors Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.;  
Suda, T.

#journal Oncogene (1994) 9:1155-1161

#title Molecular cloning of a novel non-receptor tyrosine kinase,  
HYL (hematopoietic consensus tyrosine-lacking kinase).

#accession S43533

##status preliminary

##molecule\_type mRNA

##residues 1-507 ##label SAK

##cross-references EMBL:X77278

GENETICS

#gene GDB:MATK  
 ##cross-references GDB:G00-304-667  
 CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3 homology  
 KEYWORDS phosphotransferase  
 FEATURE  
   55-105           #domain SH3 homology #label SH31\  
   122-211        #domain SH2 homology #label SH2\  
   233-485        #domain protein kinase homology #label KIN  
 SUMMARY         #length 507 #molecular-weight 56469 #checksum 6051  
  
 Query Match       100.0%; Score 92; DB 4; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 4.02e-08;  
 Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   493 gqdadgstsprsqep 507  
      |||||  
 Qy   493 GQDADGSTSPRSQEP 507

RESULT   2  
 ENTRY     B55625    #type complete  
 TITLE     protein-tyrosine kinase (EC 2.7.1.112),  
           megakaryocyte-associated - mouse  
 ORGANISM   #formal\_name Mus musculus #common\_name house mouse  
 DATE       24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change  
           19-Oct-1995  
 ACCESSIONS B55625  
 REFERENCE  A55625  
   #authors   Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,  
              L.L.; White, R.A.; Avraham, H.  
   #journal   J. Biol. Chem. (1995) 270:1833-1842  
   #title     Structural and functional studies of the intracellular  
              tyrosine kinase MATK gene and its translated product.  
   #accession B55625  
   ##status   preliminary; not compared with conceptual translation  
   ##molecule\_type mRNA  
   ##residues  1-465 ##label AVR  
 CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2 homology  
 KEYWORDS   phosphotransferase  
 FEATURE  
   13-63           #domain SH3 homology #label SH31\  
   80-169        #domain SH2 homology #label SH2\  
   191-443        #domain protein kinase homology #label KIN  
 SUMMARY     #length 465 #molecular-weight 51585 #checksum 6919  
  
 Query Match       81.5%; Score 75; DB 4; Length 465;  
 Best Local Similarity 60.0%; Pred. No. 1.99e-04;  
 Matches    9; Conservative   5; Mismatches   1; Indels   0; Gaps   0;

Db   451 gqeaegsaptrsqp 465  
      ||:|:|:|:|  
 Qy   493 GQDADGSTSPRSQEP 507

RESULT   3  
 ENTRY     I48926    #type complete  
 TITLE     protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse  
 ALTERNATE\_NAMES csk-type protein-tyrosine kinase  
 ORGANISM   #formal\_name Mus musculus #common\_name house mouse  
 DATE       15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change  
           15-Mar-1996  
 ACCESSIONS I48926  
 REFERENCE  A53469  
   #authors   Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.;

CC to SH2 regions of Src, Abl, Lck and p85-alpha-N (R72088-91,  
CC respectively).  
SQ Sequence 99 AA;

Query Match 31.7%; Score 187; DB 13; Length 99;  
Best Local Similarity 32.9%; Pred. No. 1.98e-09;  
Matches 25; Conservative 23; Mismatches 27; Indels 1; Gaps 1;

```

Db      5 wyugdisreevnek1rldadtglvrdestknhgdytltlrkggnklikifhrdgygf 64
      | : | | : | : | : | | | | : : | | | : | : : : | | | :
Qy     122 WFHGKISGQEA VQQLQPPEDGLFLVRE-SARHPGDYVLCVSFGRDVIHYRVLHRDGH LTI 180

Db      65 sdpltfnsvvelinhy 80
      : : | : : : : : | |
Qy     181 DEAVFFCNLM DMVEHY 196

```

Search completed: Mon Feb 3 17:02:02 1997  
Job time : 6 secs.

\*\*\*\*\*

THE FIVE (TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

```
Run on:      Mon Feb  3 17:01:07 1997; MasPar time 4.29 Seconds
              450.074 Million cell updates/sec
Tabular output not generated.
```

```
Title:           >US-08-426-509-2
Description:     (122-196) from US08426509.pep (3 of 4)
Perfect Score:  590
Sequence:       1 WFHGKISGQEAVALPPED.....HLTIDEAVFFCNLMQVVEHY 75
```

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

```
Database:      pir48
               1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
               8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc
               14:unrev
```

Statistics: Mean 38.199; Variance 81.461; scale 0.469

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	%		Query		DB	ID	Description	Pred. No.
	No.	Score	Match	Length				
1	590	100.0	507	4	A55625	protein-tyrosine kin	4.42e-89	
2	590	100.0	527	11	A49865	protein-tyrosine kin	4.42e-89	
3	570	96.6	465	4	B55625	protein-tyrosine kin	2.92e-85	
4	570	96.6	465	12	I48926	protein-tyrosine kin	2.92e-85	
5	350	59.3	450	1	JH0559	protein-tyrosine kin	5.07e-44	
6	349	59.2	450	12	I48929	protein-tyrosine kin	7.73e-44	
7	349	59.2	450	1	S15094	protein-tyrosine kin	7.73e-44	
8	344	58.3	450	4	A41973	protein-tyrosine kin	6.33e-43	
9	215	36.4	723	12	B38749	3-phosphatidylinosit	4.48e-20	
10	202	34.2	451	12	S49016	tyrosine kinase - hu	7.01e-18	
11	199	33.7	217	12	A54688	modular adaptor Grb2	2.23e-17	
12	199	33.7	217	11	A43321	growth factor recept	2.23e-17	
13	199	33.7	217	12	S26050	gene ash protein - r	2.23e-17	
14	195	33.1	841	11	A43254	protein-tyrosine-pho	1.04e-16	
15	194	32.9	217	11	JT0664	growth factor recept	1.52e-16	
16	192	32.5	724	11	A38748	3-phosphatidylinosit	3.27e-16	
17	191	32.4	239	12	A46243	epidermal growth fac	4.79e-16	
18	191	32.4	612	11	JC2197	protein-tyrosine kin	4.79e-16	
19	191	32.4	635	11	JC2198	protein-tyrosine kin	4.79e-16	
20	191	32.4	635	11	A53596	protein-tyrosine kin	4.79e-16	
21	187	31.7	628	12	S57436	protein-tyrosine kin	2.19e-15	
22	187	31.7	724	12	A38747	phosphatidylinositol	2.19e-15	
23	187	31.7	724	12	A38749	3-phosphatidylinosit	2.19e-15	
24	185	31.4	204	5	B45022	CRK-I - human	4.68e-15	
25	185	31.4	304	5	A45022	CRK-II - human	4.68e-15	
26	180	30.5	303	5	S41754	CRKL protein - human	3.09e-14	
27	180	30.5	605	12	B56707	protein-tyrosine kin	3.09e-14	
28	180	30.5	628	12	A56707	protein-tyrosine kin	3.09e-14	
29	178	30.2	303	12	S58352	SH2/SH3 adaptor prot	6.56e-14	
30	178	30.2	557	10	A00629	protein-tyrosine kin	6.56e-14	
31	174	29.5	209	11	A48090	alpha 2-chimerin, p4	2.93e-13	
32	173	29.3	870	11	B40121	GTPase-activating pr	4.26e-13	
33	173	29.3	1047	11	A40121	GTPase-activating pr	4.26e-13	
34	172	29.2	1038	12	JT0663	ras GTPase-activatin	6.18e-13	
35	172	29.2	1044	12	S01966	GTPase-activating pr	6.18e-13	
36	171	29.0	535	12	C46243	epidermal growth fac	8.96e-13	
37	169	28.6	505	4	S24550	protein-tyrosine kin	1.88e-12	
38	166	28.1	443	12	B53764	beta2-chimaerin, cer	5.70e-12	
39	166	28.1	466	11	A53764	beta2-chimaerin, cer	5.70e-12	
40	166	28.1	628	12	A40802	protein-tyrosine kin	5.70e-12	
41	164	27.8	1236	10	A53970	1-phosphatidylinosit	1.19e-11	
42	162	27.5	232	2	TVFV10	transforming protein	2.48e-11	
43	162	27.5	305	5	A49011	c-Crk - chicken	2.48e-11	
44	161	27.3	211	10	A46444	SH2-SH3 adaptor prot	3.57e-11	
45	161	27.3	595	4	A55651	protein-tyrosine-pho	3.57e-11	

## ALIGNMENTS

RESULT 1  
 ENTRY A55625 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112),  
 megakaryocyte-associated - human  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change  
 01-Mar-1996  
 ACCESSIONS A55625; S43533  
 REFERENCE A55625  
 #authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,  
 L.L.; White, R.A.; Avraham, H.  
 #journal J. Biol. Chem. (1995) 270:1877-1882

#title Structural and functional studies of the intracellular  
 tyrosine kinase MATK gene and its translated product.  
 #accession A55625  
 ##status preliminary; not compared with conceptual translation  
 ##molecule\_type DNA  
 ##residues 1-507 ##label AVR  
 REFERENCE S43533  
 #authors Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.;  
 Suda, T.  
 #journal Oncogene (1994) 9:1155-1161  
 #title Molecular cloning of a novel non-receptor tyrosine kinase,  
 HYL (hematopoietic consensus tyrosine-lacking kinase).  
 #accession S43533  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-507 ##label SAK  
 ##cross-references EMBL:X77278  
 GENETICS  
 #gene GDB:MATK  
 ##cross-references GDB:G00-304-667  
 CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3  
 homology  
 KEYWORDS phosphotransferase  
 FEATURE  
 55-105 #domain SH3 homology #label SH31\  
 122-211 #domain SH2 homology #label SH2\  
 233-485 #domain protein kinase homology #label KIN  
 SUMMARY #length 507 #molecular-weight 56469 #checksum 6051

Query Match 100.0%; Score 590; DB 4; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 4.42e-89;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 122 wfhgkisgqeavqqlppedglflvresarhpgdyvlcvsfgrdvihyrvlhrdghltid 181  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 122 WFHGKISGQEAVQQLPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGH LTID 181  
 Db 182 eavffcnlmdavehy 196  
 |||||||||||||  
 Qy 182 EAVFFCNLMDMVEHY 196

## RESULT 2

ENTRY A49865 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) matk - human  
 ALTERNATE\_NAMES megakaryocyte-associated tryosine kinase  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 30-Jun-1995 #sequence\_revision 30-Jun-1995 #text\_change  
 19-Oct-1995  
 ACCESSIONS A49865  
 REFERENCE A49865  
 #authors Bennett, B.D.; Cowley, S.; Jiang, S.; London, R.; Deng, B.;  
 Grabarek, J.; Groopman, J.E.; Goeddel, D.V.; Avraham, H.  
 #journal J. Biol. Chem. (1994) 269:1068-1074  
 #title Identification and characterization of a novel tyrosine  
 kinase from megakaryocytes.  
 #accession A49865  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-527 ##label BEN  
 ##cross-references GB:L18974  
 CLASSIFICATION #superfamily SH2 homology; protein kinase homology; SH3  
 homology  
 KEYWORDS phosphotransferase  
 FEATURE  
 55-105 #domain SH3 homology #label SH31\

122-211 #domain SH2 homology #label SH2\  
233-484 #domain protein kinase homology #label KIN  
SUMMARY #length 527 #molecular-weight 58473 #checksum 1630

Query Match 100.0%; Score 590; DB 11; Length 527;  
Best Local Similarity 100.0%; Pred. No. 4.42e-89;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 122 wfhgkisgqeavqqlppedglflvresarhpgdyvlcvsfgrdvihyrvlhrdghltid 181  
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Qy 122 WFHGKISGQEAVQQLPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHILTID 181

Db 182 eavffcnlmdmvehy 196  
|||||  
Qy 182 EAVFFCNLMDMVEHY 196

RESULT 3

ENTRY B55625 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112),  
megakaryocyte-associated - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change  
19-Oct-1995  
ACCESSIONS B55625  
REFERENCE A55625  
#authors Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler,  
L.L.; White, R.A.; Avraham, H.  
#journal J. Biol. Chem. (1995) 270:1833-1842  
#title Structural and functional studies of the intracellular  
tyrosine kinase MATK gene and its translated product.  
#accession B55625  
##status preliminary; not compared with conceptual translation  
##molecule\_type mRNA  
##residues 1-465 ##label AVR  
CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2  
homology  
KEYWORDS phosphotransferase  
FEATURE  
13-63 #domain SH3 homology #label SH31\  
80-169 #domain SH2 homology #label SH2\  
191-443 #domain protein kinase homology #label KIN  
SUMMARY #length 465 #molecular-weight 51585 #checksum 6919

Query Match 96.6%; Score 570; DB 4; Length 465;  
Best Local Similarity 97.3%; Pred. No. 2.92e-85;  
Matches 73; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 80 wfhgkisgqeaqqqlppedglflvresarhpgdyvlcvsfgrdvihyrvlhrdghltid 139  
|||||  
Qy 122 WFHGKISGQEAVQQLPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHILTID 181

Db 140 eavcfcnlmdmvehy 154  
||| |||||  
Qy 182 EAVFFCNLMDMVEHY 196

RESULT 4

ENTRY 148926 #type complete  
TITLE protein-tyrosine kinase (EC 2.7.1.112) Ctk - mouse  
ALTERNATE\_NAMES csk-type protein-tyrosine kinase  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change  
15-Mar-1996  
ACCESSIONS 148926  
REFERENCE A53469

#authors Klages, S.; Adam, D.; Class, K.; Fagnoli, J.; Bolen, J.B.;  
 Penhallow, R.C.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2597-2601  
 #title Ctk: a protein-tyrosine kinase related to Csk that defines an  
 enzyme family.  
 #cross-references NUID:94195789  
 #accession I48926  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-465 ##label RES  
 ##cross-references EMBL:U05210; NID:g450232; CDS\_PID:g450233  
 KEYWORDS phosphotransferase  
 SUMMARY #length 465 #molecular-weight 51495 #checksum 6748

Query Match 96.6%; Score 570; DB 12; Length 465;  
 Best Local Similarity 97.3%; Pred. No. 2.92e-85;  
 Matches 73; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 80 wfhgkisgqeaiqlppedglflvresarhpgdyvlcvsfgrdvihyrvlhrdghltid 139  
 |||||:|||||  
 Qy 122 WFHGKISGQEAQQQLQPPEDGLFLVRESARHPCDYVLCVSFGRDVIHYRVLHRDGH LTID 181  
 Db 140 eavcfcnlmdavehy 154  
 ||| |||||  
 Qy 182 EAVFFCNLMDMVEHY 196

# RESULT 5

ENTRY JH0559 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) CSK - human  
 ALTERNATE\_NAMES protein-tyrosine kinase cyl; protein-tyrosine kinase T2  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 30-Jun-1992 #sequence\_revision 20-Aug-1994 #text\_change  
 16-Feb-1996  
 ACCESSIONS JH0559; S38818; S19024; S19025  
 REFERENCE JH0559  
 #authors Braeuninger, A.; Holtrich, U.; Strebhardt, K.;  
 Ruebsaenen-Waigmann, H.  
 #journal Gene (1992) 110:205-211  
 #title Isolation and characterization of a human gene that encodes a  
 new subclass of protein tyrosine kinases.  
 #cross-references NUID:92165060  
 #accession JH0559  
 ##molecule\_type mRNA  
 ##residues 1-450 ##label BRA  
 ##cross-references EMBL:X59932  
 ##experimental\_source lung  
 REFERENCE S38818  
 #authors Braeuninger, A.; Karn, T.; Strebhardt, K.;  
 Ruebsaenen-Waigmann, H.  
 #journal Oncogene (1993) 8:1365-1369  
 #title Characterization of the human CSK locus.  
 #accession S38818  
 ##status preliminary  
 ##molecule\_type DNA  
 ##residues 1-450 ##label BR2  
 ##cross-references EMBL:X74765  
 REFERENCE S19024  
 #authors Partanen, J.; Armstrong, E.; Bergman, M.; Maekela, T.P.;  
 Hirvonen, H.; Huebner, K.; Alitalo, K.  
 #journal Oncogene (1991) 6:2013-2018  
 #title cyl encodes a putative cytoplasmic tyrosine kinase lacking  
 the conserved tyrosine autophosphorylation site (Y416  
 (src)).  
 #cross-references NUID:92050797  
 #accession S19024

Run on: Mon Feb 3 17:11:18 1997; MasPar time 9.20 Seconds  
671.122 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-6  
Description: (247-486) from US08426509.pep (3 of 3)  
Perfect Score: 1791  
Sequence: 1 GSGQFGEVWGLWNNTTPVA.....QFYINIMLECWNAEPKERPTF 240

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 45.069; Variance 114.513; scale 0.394

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1775	99.1	505	11	I38396	protein-tyrosine kin	8.20e-266	
2	1272	71.0	505	4	S24550	protein-tyrosine kin	2.96e-182	
3	1268	70.8	506	4	S24553	protein-tyrosine kin	1.35e-181	
4	1203	67.2	362	4	S24551	protein-tyrosine kin	7.25e-171	
5	1189	66.4	334	4	S24552	protein-tyrosine kin	1.47e-168	
6	1114	62.2	509	1	TVHAST	protein-tyrosine kin	3.27e-156	
7	1089	60.8	507	4	A39939	protein-tyrosine kin	4.20e-152	
8	1074	60.0	536	4	S33569	protein-tyrosine kin	1.22e-149	
9	1070	59.7	512	4	A39719	protein-tyrosine kin	5.54e-149	
10	1070	59.7	512	1	TVHULY	protein-tyrosine kin	5.54e-149	
11	1063	59.4	539	11	B49114	protein-tyrosine kin	7.81e-148	
12	1060	59.2	542	11	A49114	protein-tyrosine kin	2.43e-147	
13	1056	59.0	532	4	A34104	protein-tyrosine kin	1.10e-146	
14	1056	59.0	532	4	B34104	protein-tyrosine kin	1.10e-146	
15	1051	58.7	505	1	TVHUHC	protein-tyrosine kin	7.27e-146	
16	1051	58.7	542	1	TVHUSC	protein-tyrosine kin	7.27e-146	
17	1049	58.6	541	4	A43610	protein-tyrosine kin	1.55e-145	
18	1045	58.3	526	4	S15582	protein-tyrosine kin	7.00e-145	
19	1044	58.3	557	1	TVFVS2	protein-tyrosine kin	1.02e-144	
20	1044	58.3	587	1	TVFVPR	protein-tyrosine kin	1.02e-144	
21	1043	58.2	526	1	TVFV60	protein-tyrosine kin	1.49e-144	
22	1042	58.2	526	1	TVFVR	protein-tyrosine kin	2.17e-144	
23	1043	58.2	533	1	TVCHS	protein-tyrosine kin	1.49e-144	
24	1040	58.1	503	1	TVMSHC	protein-tyrosine kin	4.63e-144	
25	1040	58.1	537	4	A43806	protein-tyrosine kin	4.63e-144	
26	1039	58.0	526	4	S20808	protein-tyrosine kin	6.75e-144	
27	1039	58.0	526	1	OKFVYR	protein-tyrosine kin	6.75e-144	
28	1038	58.0	568	1	TVFVS1	protein-tyrosine kin	9.84e-144	
29	1037	57.9	509	4	A23639	protein-tyrosine kin	1.44e-143	
30	1035	57.8	503	4	J01321	protein-tyrosine kin	3.05e-143	
31	1036	57.8	537	1	TVHUSY	protein-tyrosine kin	2.09e-143	
32	1034	57.7	392	4	S04205	protein-tyrosine kin	4.45e-143	

33	1034	57.7	523	1	TVFVMT	protein-tyrosine kin	4.45e-143
34	1032	57.6	526	7	S20676	protein-tyrosine kin	9.47e-143
35	1032	57.6	526	7	S26420	src protein - Rous s	9.47e-143
36	1030	57.5	509	1	OKHULK	protein-tyrosine kin	2.02e-142
37	1029	57.5	537	1	TVHUSR	protein-tyrosine kin	2.94e-142
38	1026	57.3	663	1	TVMVRR	protein-tyrosine kin	9.12e-142
39	1024	57.2	529	1	TVHUFR	protein-tyrosine kin	1.94e-141
40	1022	57.1	517	12	S24547	protein-tyrosine kin	4.12e-141
41	1022	57.1	541	1	TVCHYS	protein-tyrosine kin	4.12e-141
42	1023	57.1	545	7	S52313	pp62v protein - Rous	2.83e-141
43	1022	57.1	546	7	S52314	pp62v protein - Rous	4.12e-141
44	1016	56.7	537	4	A45501	protein-tyrosine kin	3.96e-140
45	1016	56.7	541	12	S31645	protein-tyrosine kin	3.96e-140

# ALIGNMENTS

RESULT 1

ENTRY 138396 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) FRK - human  
 ALTERNATE\_NAMES FYN-related kinase (FRK)  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 15-Mar-1996  
 ACCESSIONS 138396  
 REFERENCE 138396  
 #authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.  
 #journal Gene (1994) 138:247-251  
 #title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.  
 #cross-references MUID:94171047  
 #accession 138396  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-505 ##label RES  
 ##cross-references EMBL:U00803; NID:g392887; CDS\_PID:g392888  
 GENETICS  
 #gene GDB:FRK  
 ##cross-references GDB:G00-355-675  
 KEYWORDS phosphotransferase  
 SUMMARY #length 505 #molecular-weight 58254 #checksum 9379

Query Match 99.1%; Score 1775; DB 11; Length 505;  
 Best Local Similarity 99.6%; Pred. No. 8.20e-266;  
 Matches 239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db	241	gsgqfgevweglwnnttpvavktlkpgsmdpndflreaqimknlrhpkliqlyavctled	300
Qy	247	GSGQFGEVWEGLWNNTTPVAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAVCTLED	306
Db	301	piyiitelmrhgsllqeylqndtgskihltqqvdnaaqvasgnaylesrnyihrdlaarnv	360
Qy	307	PIYIITELMRHGSLLQEYLQNDTGSKIHLTQQYDMAAQVASGNAYLESRNYIHRDLAARNV	366
Db	361	lvgehniykvadfglarvfkvdnediyesrheiklpvkwtapeairsnkfsiksdvwsfg	420
Qy	367	LVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSDVWSFG	426
Db	421	illyeiitygkmpysgmtgaqvinqlaqnyrlpqpsncpqfynimlecwnaepkerptf	480
Qy	427	ILLYEITYGKMPYSGMTGAQVIQMLAQNYRLPQPSNCPQFYNIMLECWNAEPKERPTF	486

RESULT 2

ENTRY S24550 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) 1 - freshwater sponge

(Spongilla lacustris)

ALTERNATE\_NAMES src-type tyrosine kinase 1  
 ORGANISM #formal\_name Spongilla lacustris  
 DATE 07-May-1993 #sequence\_revision 07-May-1993 #text\_change  
 03-Nov-1995

ACCESSIONS S24550  
 REFERENCE S24550  
 #authors Raulf, F.  
 #submission submitted to the EMBL Data Library, September 1991  
 #accession S24550  
 ##molecule\_type mRNA  
 ##residues 1-505 ##label RAU  
 ##cross-references EMBL:X61601

GENETICS  
 #gene srk1

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase  
 homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase

FEATURE  
 61-111 #domain SH3 homology #label SH3\  
 122-214 #domain SH2 homology #label SH2\  
 238-496 #domain protein kinase homology #label KIN\  
 246-254 #region protein kinase ATP-binding motif\  
 268 #active\_site Lys #status predicted

SUMMARY #length 505 #molecular-weight 57693 #checksum 3389

Query Match 71.0%; Score 1272; DB 4; Length 505;  
 Best Local Similarity 67.5%; Pred. No. 2.96e-182;  
 Matches 162; Conservative 40; Mismatches 34; Indels 4; Gaps 3;

Db 247 gagqfgevweglungttsvavktlkpgtmsveeflqeasimkrlrhpklilyavctkee 306  
 |:||||||| |:|||||||:| ::||:| ||| ||||||||| |:|  
 Qy 247 GSGQFGEVWEGLWNNITPVAVKTLKPGSMDPNDFLEAQIMKNLRHPKLIQLYAVCTLED 306

Db 307 piyivtelmkyslleylrgedgv-lkieqlvdvaaqvasgnsyleqqnyihrdlaarni 365  
 ||||:||||: ||| |||: | : : | |:|||||||:||| :|||||||:  
 Qy 307 PIYIITELMRHCSLQEYLDNDTGSKIHLTQ@YDMAAQVASGMAYLESRNYIHRDLAARNV 366

Db 366 lvgehickvadfglarv--id-eeiyeahtgakfpikwtapeaanynrftiksdvwsfg 422  
 ||||| | ||||||||| :| |:|||:| |:|:||||||| |:|:|||||||  
 Qy 367 LVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSDVWSFG 426

Db 423 vlyeiitygrfpypgntnpevlekiqqnyrnpcpancpkqfhdmldcwredpasrptf 482  
 ::||||||| |:||| :|:|:|:| ||||:| |:||| || :|||:| :| ||||  
 Qy 427 ILLYEIITYGKMPYSGNTGAQVIQMLAQNYRLPQPSNCPQ@FYINIMLECWNAEPKERPTF 486

RESULT 3

ENTRY S24553 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) 4 - freshwater sponge  
 (Spongilla lacustris)

ALTERNATE\_NAMES src-type tyrosine kinase 4  
 ORGANISM #formal\_name Spongilla lacustris  
 DATE 07-May-1993 #sequence\_revision 07-May-1993 #text\_change  
 03-Nov-1995

ACCESSIONS S24553  
 REFERENCE S24550  
 #authors Raulf, F.  
 #submission submitted to the EMBL Data Library, September 1991  
 #accession S24553  
 ##molecule\_type mRNA  
 ##residues 1-506 ##label RAU  
 ##cross-references EMBL:X61604

GENETICS  
 #gene srk4

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase

homology; SH2 homology; SH3 homology  
 KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase  
 FEATURE  
 61-111 #domain SH3 homology #label SH3\  
 122-214 #domain SH2 homology #label SH2\  
 238-496 #domain protein kinase homology #label KIN\  
 246-254 #region protein kinase ATP-binding motif\  
 268 #active\_site Lys #status predicted  
 SUMMARY #length 506 #molecular-weight 57561 #checksum 9002

Query Match 70.8%; Score 1268; DB 4; Length 506;  
 Best Local Similarity 66.7%; Pred. No. 1.35e-181;  
 Matches 160; Conservative 40; Mismatches 36; Indels 4; Gaps 3;

Db 247 gagqfgevweglungttsvavktlkpgtmsieefleeasimkqlrhpqliqlyavctkee 306  
 |:||||| |:|||||:| :|| ||| ||||| |:|  
 Qy 247 GSGQFGEVWEGLNWNTTPVAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAVCTLED 306

Db 307 piyivtelmkhgsllleylrgd-grsklpdlvdacsqvasgmsyleqqnyihrdlaarni 365  
 ||||:||||:|||| |:| :| :| :| :|||:| |:| |||||:  
 Qy 307 PIYIITELMRHGSLSQEYLQNDTGSKIHLTQQYDMAAQVASGMAYLESRNYIHRDLAARNV 366

Db 366 lvgehkckvadfglarv--id-eeiyeaklgakfpikutapeaanysrftiksdvwsfg 422  
 ||||:| ||||| |:| |:|:| |:|:| |:|:| |:|:|  
 Qy 367 LVGEHNIYKVADFGLARVFKVDNEDIYESRHEIKLPVKWTAPEAIRSNKFSIKSDVWSFG 426

Db 423 ivlyevitygrfpypgntnaqvleqiqqsyrmprmgcpeklgammaadwredpasrptf 482  
 |:|:|:| |:|:| |:|:| :|:|:| |:|:| |:|:| |:|:| :|  
 Qy 427 ILLYEIITYGKMPYSGMTGAQVIQMLAQNYRLPQPSNCPQGFYNIMLECWNAEPKERPTF 486

RESULT 4  
 ENTRY S24551 #type fragment  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) 2 - freshwater sponge  
 (Spongilla lacustris) (fragment)  
 ALTERNATE\_NAMES src-type tyrosine kinase 2  
 ORGANISM #formal\_name Spongilla lacustris  
 DATE 07-May-1993 #sequence\_revision 07-May-1993 #text\_change  
 03-Nov-1995  
 ACCESSIONS S24551  
 REFERENCE S24550  
 #authors Raulf, F.  
 #submission submitted to the EMBL Data Library, September 1991  
 #accession S24551  
 ##molecule\_type mRNA  
 ##residues 1-362 ##label RAU  
 ##cross-references EMBL:X61602

GENETICS  
 #gene srk2  
 CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase  
 homology; SH2 homology; SH3 homology  
 KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase  
 FEATURE  
 1-70 #domain SH2 homology (fragment) #label SH2\  
 93-351 #domain protein kinase homology #label KIN\  
 101-109 #region protein kinase ATP-binding motif\  
 123 #active\_site Lys #status predicted  
 SUMMARY #length 362 #checksum 2776

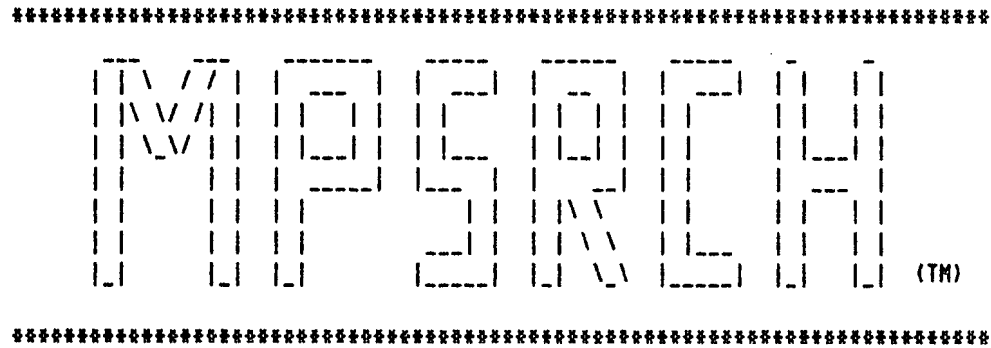
Query Match 67.2%; Score 1203; DB 4; Length 362;  
 Best Local Similarity 64.6%; Pred. No. 7.25e-171;  
 Matches 155; Conservative 44; Mismatches 37; Indels 4; Gaps 4;

Db 102 gagqfgevvyqglunnstpvavktlkagtnqpaaflaeqimkklrhpqliqlyavctqge 161  
 |:||||| |:|:|:| |:|:|:| |:|:| ||| |:|:|:| |:|:| :|  
 Qy 247 GSGQFGEVWEGLNWNTTPVAVKTLKPGSMDPNDFLREAQIMKNLRHPKLIQLYAVCTLED 306

Query Match 24.3%; Score 107; DB 9; Length 48;  
 Best Local Similarity 53.6%; Pred. No. 4.51e-02;  
 Matches 15; Conservative 7; Mismatches 4; Indels 2; Gaps 2;

Db 6 alydyearteddlsfekgek-fq-nedl 31  
 ||:|:| | :| | | | :| :| :| :|  
 Qy 54 ALFDYQARTAEDLSFRAGDKKLQVLDL 81

Search completed: Mon Feb 3 17:10:17 1997  
 Job time : 9 secs.



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:09:24 1997; MasPar time 3.90 Seconds  
 389.446 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-6  
 Description: (54-112) from US08426509.pep (2 of 3)  
 Perfect Score: 440  
 Sequence: 1 ALFDYQARTAEDLSFRAGDK.....KRRDGSSQQLQGYIPSNYVA 59

Scoring table: PAM 150  
 Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: pir48  
 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
 14:unrev

Statistics: Mean 36.207; Variance 80.441; scale 0.450

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Pred. No.
	No.	Score	Match	Length	DB	ID	
1	422	95.9	505	11	138396	protein-tyrosine kin	6.98e-56
2	191	43.4	509	1	TVHAST	protein-tyrosine kin	6.03e-16

3	170	38.6	532	4	B34104	protein-tyrosine kin	1.33e-12
4	167	38.0	542	11	A49114	protein-tyrosine kin	3.92e-12
5	166	37.7	534	4	A44991	protein-tyrosine kin	5.62e-12
6	166	37.7	534	4	S33568	protein-tyrosine kin	5.62e-12
7	166	37.7	537	1	TVHUSY	protein-tyrosine kin	5.62e-12
8	166	37.7	537	1	TVHUSR	protein-tyrosine kin	5.62e-12
9	166	37.7	537	4	A45501	protein-tyrosine kin	5.62e-12
10	165	37.5	532	4	A34104	protein-tyrosine kin	8.04e-12
11	165	37.5	537	4	A43806	protein-tyrosine kin	8.04e-12
12	165	37.5	543	1	TVHUYS	protein-tyrosine kin	8.04e-12
13	162	36.8	541	12	S31645	protein-tyrosine kin	2.36e-11
14	161	36.6	517	12	S24547	protein-tyrosine kin	3.37e-11
15	160	36.4	528	1	TVFVG9	protein-tyrosine kin	4.81e-11
16	160	36.4	529	1	TVHUFR	protein-tyrosine kin	4.81e-11
17	160	36.4	541	1	TVCHYS	protein-tyrosine kin	4.81e-11
18	158	35.9	533	1	TVCHS	protein-tyrosine kin	9.79e-11
19	158	35.9	539	11	B49114	protein-tyrosine kin	9.79e-11
20	158	35.9	557	1	TVFVS2	protein-tyrosine kin	9.79e-11
21	158	35.9	568	1	TVFVS1	protein-tyrosine kin	9.79e-11
22	158	35.9	587	1	TVFVPR	protein-tyrosine kin	9.79e-11
23	157	35.7	451	12	S49016	tyrosine kinase - hu	1.40e-10
24	156	35.5	536	4	S33569	protein-tyrosine kin	1.99e-10
25	153	34.8	505	4	S24550	protein-tyrosine kin	5.73e-10
26	153	34.8	506	4	S24553	protein-tyrosine kin	5.73e-10
27	153	34.8	517	4	A43807	protein-tyrosine kin	5.73e-10
28	152	34.5	512	4	A39719	protein-tyrosine kin	8.14e-10
29	151	34.3	526	4	S20808	protein-tyrosine kin	1.16e-09
30	151	34.3	526	4	S15582	protein-tyrosine kin	1.16e-09
31	151	34.3	526	1	TVFVR	protein-tyrosine kin	1.16e-09
32	151	34.3	526	1	OKFVYR	protein-tyrosine kin	1.16e-09
33	147	33.4	505	1	TVHUHC	protein-tyrosine kin	4.68e-09
34	146	33.2	526	1	TVFV60	protein-tyrosine kin	6.62e-09
35	145	33.0	907	9	A57087	cell division contro	9.37e-09
36	144	32.7	503	1	TVMSHC	protein-tyrosine kin	1.32e-08
37	144	32.7	512	1	TVHULY	protein-tyrosine kin	1.32e-08
38	143	32.5	526	7	S20676	protein-tyrosine kin	1.87e-08
39	143	32.5	526	7	S26420	src protein - Rous s	1.87e-08
40	142	32.3	503	4	J01321	protein-tyrosine kin	2.64e-08
41	140	31.8	545	7	S52313	pp62v protein - Rous	5.25e-08
42	140	31.8	546	7	S52314	pp62v protein - Rous	5.25e-08
43	131	29.8	303	5	S41754	CRKL protein - human	1.12e-06
44	130	29.5	259	5	A44988	transforming protein	1.56e-06
45	130	29.5	305	5	A49011	c-Crk - chicken	1.56e-06

# ALIGNMENTS

RESULT 1

ENTRY I38396 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) FRK - human

ALTERNATE\_NAMES FYN-related kinase (FRK)

ORGANISM #formal\_name Homo sapiens #common\_name nan

DATE 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 15-Mar-1996

ACCESSIONS I38396

REFERENCE I38396

#authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.

#journal Gene (1994) 138:247-251

#title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.

#cross-references MUID:94171047

#accession I38396

##status preliminary

##molecule\_type mRNA

##residues 1-505 ##label RES

##cross-references EMBL:U00803; NID:a392887; CDS PID:a392888

## GENETICS

#gene GDB:FRK  
 ##cross-references GDB:G00-355-675  
 KEYWORDS phosphotransferase  
 SUMMARY #length 505 #molecular-weight 58254 #checksum 9379

Query Match 95.9%; Score 422; DB 11; Length 505;  
 Best Local Similarity 98.3%; Pred. No. 6.98e-56;  
 Matches 58; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 49 alfdyqartaedlsfragdk-lqvldtlhegwufarhlekrddgssqqlqgyipsnyva 106  
 |||||  
 Qy 54 ALFDYQARTAEDLSFRAGDKKLQVLDLHEGWUFARHLEKRRDGSSQQLQGYIPSNYVA 112

## RESULT 2

ENTRY TVHAST #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) stk - Hydra attenuata  
 ORGANISM #formal\_name Hydra attenuata  
 DATE 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change  
 20-Aug-1994  
 ACCESSIONS A34094  
 REFERENCE A34094  
 #authors Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E.  
 #journal Mol. Cell. Biol. (1989) 9:4141-4151  
 #title Structure and expression of STK, a src-related gene in the  
 simple metazoan Hydra attenuata.  
 #cross-references MUID:90066418  
 #accession A34094  
 ##molecule\_type mRNA  
 ##residues 1-509 ##label BOS  
 ##cross-references GB:M25245

## GENETICS

#gene stk  
 CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase  
 homology; SH2 homology; SH3 homology  
 KEYWORDS ATP; phosphoprotein; phosphotransferase; transforming  
 protein; tyrosine-specific protein kinase

## FEATURE

66-115 #domain SH3 homology #label SH3\  
 126-218 #domain SH2 homology #label SH2\  
 238-497 #domain protein kinase homology #label KIN\  
 246-254 #region protein kinase ATP-binding motif\  
 268 #active\_site Lys #status predicted\  
 390 #binding\_site phosphate (Tyr) (covalent) (by  
 autophosphorylation) #status predicted

SUMMARY #length 509 #molecular-weight 56885 #checksum 8721

Query Match 43.4%; Score 191; DB 1; Length 509;  
 Best Local Similarity 47.7%; Pred. No. 6.03e-16;  
 Matches 21; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Db 66 alydyearisedlsfkkger-lqiintadgdwuyarsliitnseg 108  
 ||||| :||||| :: ||::| |||| | :|  
 Qy 54 ALFDYQARTAEDLSFRAGDKKLQVLDLHEGWUFARHLEKRRDG 97

## RESULT 3

ENTRY B34104 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) src 2 - African clawed  
 frog  
 ALTERNATE\_NAMES kinase-related transforming protein (src); kinase-related  
 transforming protein (src) 2  
 ORGANISM #formal\_name Xenopus laevis #common\_name African clawed frog  
 DATE 30-Mar-1990 #sequence\_revision 30-Mar-1990 #text\_change  
 09-Sep-1994

ACCESSIONS B34104  
 REFERENCE A34104  
 #authors Steele, R.E.; Unger, T.F.; Mardis, M.J.; Fero, J.B.  
 #journal J. Biol. Chem. (1989) 264:10649-10653  
 #title The two *Xenopus laevis* SRC genes are co-expressed and each produces functional pp(60src).  
 #cross-references MUID:89278134  
 #accession B34104  
 ##status preliminary; not compared with conceptual translation  
 ##molecule\_type mRNA  
 ##residues 1-532 ##label STE  
 CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology  
 KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase  
 FEATURE  
 87-136 #domain SH3 homology #label SH3\  
 147-244 #domain SH2 homology #label SH2\  
 264-522 #domain protein kinase homology #label KIN\  
 272-280 #region protein kinase ATP-binding motif  
 SUMMARY #length 532 #molecular-weight 59736 #checksum 7595

Query Match 38.6%; Score 170; DB 4; Length 532;  
 Best Local Similarity 50.0%; Pred. No. 1.33e-12;  
 Matches 19; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

Db 87 alydyesrtetdlsfrkger-lqivnnategdwuarsl 123  
 ||:||||| |||| |:: ||::: ||:| |  
 Qy 54 ALFDYQARTAEDLSFRAGDKKLQVLDLHEGWWFARHL 91

RESULT 4  
 ENTRY A49114 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) fyn - Pacific electric ray  
 ORGANISM #formal\_name *Torpedo californica* #common\_name Pacific electric ray  
 DATE 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 19-Jan-1996  
 ACCESSIONS A49114  
 REFERENCE A49114  
 #authors Swope, S.L.; Huganir, R.L.  
 #journal J. Biol. Chem. (1993) 268:25152-25161  
 #title Molecular cloning of two abundant protein tyrosine kinases in *Torpedo* electric organ that associate with the acetylcholine receptor.  
 #accession A49114  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-542 ##label SWO  
 ##cross-references GB:U01349  
 CLASSIFICATION #superfamily protein kinase homology; SH3 homology  
 KEYWORDS phosphotransferase  
 FEATURE  
 94-143 #domain SH3 homology #label SH3\  
 274-532 #domain protein kinase homology #label KIN  
 SUMMARY #length 542 #molecular-weight 61096 #checksum 2657

Query Match 38.0%; Score 167; DB 11; Length 542;  
 Best Local Similarity 51.3%; Pred. No. 3.92e-12;  
 Matches 20; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

Db 94 alydydartdddsfhhgek-fqilnnategdwuearsiq 131  
 ||:||||| :||||: |:| :|:: || || |  
 Qy 54 ALFDYQARTAEDLSFRAGDKKLQVLDLHEGWWFARHLE 92

(TM)

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```
Run on:      Mon Feb  3 16:55:24 1997;  MasPar time 4.55 Seconds
           452.373 Million cell updates/sec
```

```
Title:          >US-08-426-509-6
Description:    (122-201) from US08426509.pep (1 of 3)
Perfect Score: 586
Sequence:      1 WFFGAIGRSDAEKQLLYSEN.....FLTRRRIFSTLNEFVSHYTK 80
```

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Statistics: Mean 38.963; Variance 91.030; scale 0.428

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	%		Query		DB	ID	Description	Pred. No.
	No.	Score	Match	Length				
1	586	100.0	505	11	I38396	protein-tyrosine kin	4.99e-80	
2	351	59.9	499	4	A40092	protein-tyrosine kin	8.16e-40	
3	347	59.2	509	1	TVHAST	protein-tyrosine kin	3.78e-39	
4	344	58.7	506	4	S24553	protein-tyrosine kin	1.19e-38	
5	334	57.0	505	4	S24550	protein-tyrosine kin	5.45e-37	
6	333	56.8	505	11	S51647	protein-tyrosine kin	7.98e-37	
7	325	55.5	505	1	TVHUNC	protein-tyrosine kin	1.68e-35	
8	320	54.6	509	1	OKHULK	protein-tyrosine kin	1.12e-34	
9	319	54.4	503	4	J01321	protein-tyrosine kin	1.64e-34	
10	319	54.4	509	4	A23639	protein-tyrosine kin	1.64e-34	
11	316	53.9	503	1	TVMSHC	protein-tyrosine kin	5.11e-34	
12	310	52.9	512	1	TVHULY	protein-tyrosine kin	4.95e-33	
13	310	52.9	526	1	TVFV60	protein-tyrosine kin	4.95e-33	
14	310	52.9	533	1	TVCHS	protein-tyrosine kin	4.95e-33	
15	310	52.9	557	1	TVFVS2	protein-tyrosine kin	4.95e-33	
16	310	52.9	568	1	TVFVS1	protein-tyrosine kin	4.95e-33	
17	310	52.9	587	1	TVFVPR	protein-tyrosine kin	4.95e-33	
18	308	52.6	541	4	A43610	protein-tyrosine kin	1.05e-32	
19	308	52.6	542	1	TVHUSC	protein-tyrosine kin	1.05e-32	

20	307	52.4	512	4	A39719	protein-tyrosine kin	1.54e-32
21	303	51.7	523	1	TVFVMT	protein-tyrosine kin	6.94e-32
22	303	51.7	534	4	S33568	protein-tyrosine kin	6.94e-32
23	303	51.7	537	1	TVHUSY	protein-tyrosine kin	6.94e-32
24	303	51.7	545	7	S52313	pp62v protein - Rous	6.94e-32
25	303	51.7	546	7	S52314	pp62v protein - Rous	6.94e-32
26	302	51.5	537	1	TVHUSR	protein-tyrosine kin	1.01e-31
27	300	51.2	534	4	A44991	protein-tyrosine kin	2.15e-31
28	299	51.0	537	4	A43806	protein-tyrosine kin	3.13e-31
29	299	51.0	541	12	S31645	protein-tyrosine kin	3.13e-31
30	299	51.0	663	1	TVMVRR	protein-tyrosine kin	3.13e-31
31	298	50.9	529	1	TVHUFR	protein-tyrosine kin	4.55e-31
32	297	50.7	536	4	S33569	protein-tyrosine kin	6.63e-31
33	297	50.7	537	4	A45501	protein-tyrosine kin	6.63e-31
34	297	50.7	543	1	TVHUYS	protein-tyrosine kin	6.63e-31
35	296	50.5	517	4	A43807	protein-tyrosine kin	9.66e-31
36	296	50.5	539	11	B49114	protein-tyrosine kin	9.66e-31
37	292	49.8	392	4	S04205	protein-tyrosine kin	4.33e-30
38	292	49.8	542	11	A49114	protein-tyrosine kin	4.33e-30
39	290	49.5	362	4	S24551	protein-tyrosine kin	9.16e-30
40	290	49.5	528	1	TVFVG9	protein-tyrosine kin	9.16e-30
41	290	49.5	541	1	TVCHYS	protein-tyrosine kin	9.16e-30
42	289	49.3	532	4	B34104	protein-tyrosine kin	1.33e-29
43	288	49.1	507	4	A39939	protein-tyrosine kin	1.94e-29
44	288	49.1	517	12	S24547	protein-tyrosine kin	1.94e-29
45	288	49.1	532	4	A34104	protein-tyrosine kin	1.94e-29

# ALIGNMENTS

RESULT 1

ENTRY 138396 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) FRK - human  
 ALTERNATE\_NAMES FYN-related kinase (FRK)  
 ORGANISM #formal\_name Homo sapiens #common\_name nan  
 DATE 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 15-Mar-1996  
 ACCESSIONS 138396  
 REFERENCE 138396  
 #authors Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.  
 #journal Gene (1994) 138:247-251  
 #title Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene.  
 #cross-references MUID:94171047  
 #accession 138396  
 ##status preliminary  
 ##molecule\_type mRNA  
 ##residues 1-505 ##label RES  
 ##cross-references EMBL:U00803; NID:g392887; CDS\_PID:g392888  
 GENETICS  
 #gene GDB:FRK.  
 ##cross-references GDB:G00-355-675  
 KEYWORDS phosphotransferase  
 SUMMARY #length 505 #molecular-weight 58254 #checksum 9379

Query Match 100.0X; Score 586; DB 11; Length 505;  
 Best Local Similarity 100.0X; Pred. No. 4.99e-80;  
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 wffgaigrsdaekqlllysenktgsflireseqkgefslsvldgavvkhyrikrldegff 175

|||||

Qy 122 WFFGAIGRSDAEKQLLYSENKTGSFLIRESESQKGEFSLSVLDGAVVKHYRIKRLDEGGF 181

Db 176 fltrrrrifstlnefvshytk 195

|||||

Qy 182 FLTRRRIFSTLNEFVSHYTK 201

RESULT 2

ENTRY A40092 #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) blk - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 09-Sep-1994

ACCESSIONS A40092

REFERENCE A40092

#authors Dynecki, S.M.; Niederhuber, J.E.; Desiderio, S.V.

#journal Science (1990) 247:332-336

#title Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.

#cross-references MUID:90117147

#accession A40092

##status preliminary

##molecule\_type mRNA

##residues 1-499 ##label DYM

##cross-references GB:M30903

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase

FEATURE

59-107 #domain SH3 homology #label SH3\

118-214 #domain SH2 homology #label SH2\

233-491 #domain protein kinase homology #label KIN\

241-249 #region protein kinase ATP-binding motif

SUMMARY #length 499 #molecular-weight 56644 #checksum 4536

Query Match 59.9%; Score 351; DB 4; Length 499;

Best Local Similarity 58.3%; Pred. No. 8.16e-40;

Matches 49; Conservative 17; Mismatches 14; Indels 4; Gaps 2;

Db 118 wffrtisrkd aerql lapankagsfliresesnkgafslsvkdittqgevvkhykirsld 177

||| :|:| :||:| | : ||:||||||| || ||||| : :| ||||:|: ||

Qy 122 WFFGAIGRSDAEKQLLYSENKTSFLIRESESQKGEFSLSV--L--DGAVVKHYRIKRLD 177

Db 178 nggyyisprifptlqalvqhysk 201

:|:|:|: | |:|| :| ||:|

Qy 178 EGGFFLTRRRIFSTLNEFVSHYTK 201

RESULT 3

ENTRY TVHAST #type complete

TITLE protein-tyrosine kinase (EC 2.7.1.112) stk - Hydra attenuata

ORGANISM #formal\_name Hydra attenuata

DATE 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 20-Aug-1994

ACCESSIONS A34094

REFERENCE A34094

#authors Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E.

#journal Mol. Cell. Biol. (1989) 9:4141-4151

#title Structure and expression of STK, a src-related gene in the simple metazoan Hydra attenuata.

#cross-references MUID:90066418

#accession A34094

##molecule\_type mRNA

##residues 1-509 ##label BOS

##cross-references GB:M25245

GENETICS

#gene stk

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphoprotein; phosphotransferase; transforming protein; tyrosine-specific protein kinase

SQ Sequence 3898 AA;

Query Match 45.9%; Score 51; DB 17; Length 3898;  
Best Local Similarity 33.3%; Pred. No. 1.94e+02;  
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 3144 hlvgdiatikekakq 3158  
:|:| | :|:| |:  
Qy 661 QLLSSIEPLREKDKH 675

Search completed: Mon Feb 3 17:08:40 1997  
Job time : 10 secs.

\*\*\*\*\*

MPsrch\_pp (TM)

\*\*\*\*\*

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:08:03 1997; MasPar time 2.69 Seconds  
153.247 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-4  
Description: (660-675) from US08426509.pep (5 of 5)  
Perfect Score: 111  
Sequence: 1 QLLSSIEPLREKDKH 16

Scoring table: PAM 150  
Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir48  
1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
14:unrev

Statistics: Mean 27.034; Variance 49.322; scale 0.548

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
	1	68	61.3	148	11	S31791	stathmin - chicken	8.00e-01

2	68	61.3	149	5	A40936	stathmin - human	8.00e-01
3	68	61.3	149	12	B48917	stathmin - mouse	8.00e-01
4	68	61.3	149	5	A34294	stathmin - rat	8.00e-01
5	68	61.3	197	7	J01271	hypothetical 21.5K p	8.00e-01
6	65	58.6	1009	9	S61174	hypothetical protein	2.28e+00
7	62	55.9	678	10	S56284	hypothetical protein	6.30e+00
8	61	55.0	993	12	S49461	synaptonemal complex	8.79e+00
9	61	55.0	993	12	S59599	synaptonemal complex	8.79e+00
10	60	54.1	192	14	JC4573	Ras2 protein - Hydra	1.22e+01
11	60	54.1	192	10	S32042	RAS1 protein - Hydra	1.22e+01
12	59	53.2	805	1	YUPDS	sucrose synthase (EC	1.70e+01
13	58	52.3	243	8	S42873	probable succinate d	2.34e+01
14	58	52.3	605	3	ABPGS	serum albumin precur	2.34e+01
15	58	52.3	681	6	A36500	transferrin precurs	2.34e+01
16	58	52.3	2470	9	S57085	1-phosphatidylinosit	2.34e+01
17	57	51.4	437	11	S15704	transforming protein	3.22e+01
18	57	51.4	708	9	S53411	hypothetical protein	3.22e+01
19	57	51.4	763	6	S55616	glycoprotein H - equ	3.22e+01
20	56	50.5	179	12	A48917	SCG10 protein - mous	4.42e+01
21	56	50.5	179	5	A36110	SCG10 protein - rat	4.42e+01
22	56	50.5	237	7	JH0671	high-affinity branch	4.42e+01
23	56	50.5	239	7	JC4346	flagellar-specific s	4.42e+01
24	56	50.5	241	7	S47673	leucine transport pr	4.42e+01
25	56	50.5	494	1	B45738	alpha-amyrase (EC 3.	4.42e+01
26	56	50.5	495	1	A45738	alpha-amyrase (EC 3.	4.42e+01
27	56	50.5	508	9	S19697	aspartic proteinase	4.42e+01
28	56	50.5	598	3	RGEENX	regulatory protein n	4.42e+01
29	56	50.5	660	12	A53618	regulatory protein N	4.42e+01
30	56	50.5	756	8	B64137	tetrahydropteroyltri	4.42e+01
31	56	50.5	808	4	S25526	sucrose synthase (EC	4.42e+01
32	56	50.5	808	4	S23543	sucrose synthase (EC	4.42e+01
33	56	50.5	985	10	A32240	REV1 protein - yeast	4.42e+01
34	56	50.5	1581	11	S49149	laminin A3 - human (	4.42e+01
35	55	49.5	238	10	S22609	hypothetical protein	6.03e+01
36	55	49.5	373	7	S15200	hydrogenase isozyme	6.03e+01
37	55	49.5	406	8	S38218	hypothetical protein	6.03e+01
38	55	49.5	407	4	A49845	5-aminolevulinate sy	6.03e+01
39	55	49.5	607	3	ABBO5	serum albumin precur	6.03e+01
40	55	49.5	607	3	ABSHS	serum albumin precur	6.03e+01
41	55	49.5	807	4	S29242	sucrose synthase (EC	6.03e+01
42	54	48.6	406	12	S27010	aminoacylase (EC 3.5	8.21e+01
43	54	48.6	802	1	YU2MS	sucrose synthase (EC	8.21e+01
44	54	48.6	1025	4	JC1266	beta-galactosidase (	8.21e+01
45	54	48.6	2016	10	S27411	cell division-associ	8.21e+01

# ALIGNMENTS

```

RESULT      1
ENTRY       S31791      #type complete
TITLE       stathmin - chicken
ORGANISM    #formal_name Gallus gallus #common_name chicken
DATE        13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
            13-Jan-1995
ACCESSIONS  S31791
REFERENCE   S20720
#authors    Godbout, R.
#submission submitted to the EMBL Data Library, April 1992
#description Identification and characterization of transcripts present at
            elevated levels in the undifferentiated chick retina.
#accession  S31791
##status    preliminary
##molecule_type mRNA
##residues  1-148 ##label GOD
##cross-references EMBL:X67840
SUMMARY     #length 148 #molecular-weight 17082 #checksum 8231

```

Query Match 61.3%; Score 68; DB 11; Length 148;  
Best Local Similarity 60.0%; Pred. No. 8.00e-01;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qnaaklerlrekdkh 129  
|: : :| |||||  
Qy 661 QLLSSIEPLREKDKH 675

RESULT 2

ENTRY A40936 #type complete  
TITLE stathmin - human  
ALTERNATE\_NAMES leukemia-associated phosphoprotein p18; oncoprotein 18; Pr22  
protein; proliferation-related phosphoprotein p18  
ORGANISM #formal\_name Homo sapiens #common\_name nan  
DATE 28-May-1992 #sequence\_revision 28-May-1992 #text\_change  
01-Mar-1996  
ACCESSIONS A40936; A44780; S31624; S10565; A39215; S42211  
REFERENCE A40936  
#authors Melhem, R.F.; Zhu, X.; Hailat, N.; Strahler, J.R.; Hanash,  
S.M.  
#journal J. Biol. Chem. (1991) 266:17747-17753  
#title Characterization of the gene for a proliferation-related  
phosphoprotein (oncoprotein 18) expressed in high amounts  
in acute leukemia.  
#cross-references MUID:92011487  
#accession A40936  
##molecule\_type DNA  
##residues 1-149 ##label MEL  
##cross-references GB:M31303  
REFERENCE A44780  
#authors Zhu, X.; Kozarsky, K.; Strahler, J.R.; Eckerskorn, C.;  
Lottspeich, F.; Melhem, R.; Lowe, J.; Fox, D.A.; Hanash,  
S.M.; Atweh, G.F.  
#journal J. Biol. Chem. (1989) 264:14556-14560  
#title Molecular cloning of a novel human leukemia-associated gene.  
Evidence of conservation in animal species.  
#accession A44780  
##molecule\_type mRNA  
##residues 1-149 ##label ZHU  
##cross-references GB:J04991  
REFERENCE S31624  
#authors Marunouchi, T.  
#submission submitted to the EMBL Data Library, January 1992  
#accession S31624  
##status preliminary  
##molecule\_type mRNA  
##residues 1-149 ##label MAR  
##cross-references EMBL:Z11566  
REFERENCE S10565  
#authors Maucuer, A.; Doye, V.; Sobel, A.  
#journal FEBS Lett. (1990) 264:275-278  
#title A single amino acid difference distinguishes the human and  
the rat sequences of stathmin, a ubiquitous intracellular  
phosphoprotein associated with cell regulations.  
#cross-references MUID:90292224  
#accession S10565  
##status preliminary  
##molecule\_type mRNA  
##residues 1-149 ##label MAU  
REFERENCE A39215  
#authors Gullberg, M.; Noreus, K.; Brattsand, G.; Friedrich, B.;  
Shingler, V.  
#journal J. Biol. Chem. (1990) 265:17499-17505  
#title Purification and characterization of a 19-kilodalton

intracellular protein. An activation-regulated putative  
protein kinase C substrate of T lymphocytes.

#cross-references MUID:91009201

#accession A39215

##molecule\_type protein

##residues 117-136 ##label GUL

REFERENCE S42211

#authors Brattsand, G.; Marklund, U.; Nylander, K.; Roos, G.;  
Gullberg, M.

#journal Eur. J. Biochem. (1994) 220:359-368

#title Cell-cycle-regulated phosphorylation of oncoprotein 18 on  
Ser16, Ser25 and Ser38.

#accession S42211

##status preliminary

##molecule\_type protein

##residues 11-44 ##label BRA

GENETICS

#gene GDB:LAP18

##cross-references GDB:G00-127-971

#map\_position 1p36.1-p35

CLASSIFICATION #superfamily stathmin

KEYWORDS cytosol; phosphoprotein

FEATURE

16,25,38 #binding\_site phosphate (Ser) (covalent) #status  
experimental

SUMMARY #length 149 #molecular-weight 17302 #checksum 1901

Query Match 61.3%; Score 68; DB 5; Length 149;

Best Local Similarity 60.0%; Pred. No. 8.00e-01;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qaaaklerlrekdkh 129

|: : :| |||||

Gy 661 QLLSSIEPLREKDKH 675

RESULT 3

ENTRY B48917 #type complete

TITLE stathmin - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 01-Dec-1995 #sequence\_revision 01-Dec-1995 #text\_change  
01-Dec-1995

ACCESSIONS B48917

REFERENCE A48917

#authors Okazaki, T.; Yoshida, B.N.; Avraham, K.B.; Wang, H.;  
Wuenschell, C.W.; Jenkins, N.A.; Copeland, N.G.; Anderson,  
D.J.; Mori, N.

#journal Genomics (1993) 18:360-373

#title Molecular diversity of the SCG10/stathmin gene family in the  
mouse.

#accession B48917

##status preliminary

##molecule\_type DNA

##residues 1-149 ##label OKA

##cross-references GB:L20258

##note authors translated the codon GAT for residue 34 as Glu

SUMMARY #length 149 #molecular-weight 17274 #checksum 2075

Query Match 61.3%; Score 68; DB 12; Length 149;

Best Local Similarity 60.0%; Pred. No. 8.00e-01;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qaaaklerlrekdkh 129

|: : :| |||||

Gy 661 QLLSSIEPLREKDKH 675

RESULT 4

ENTRY A34294 #type complete

TITLE stathmin - rat

ALTERNATE\_NAMES phosphoprotein p19

ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 18-Jun-1993

ACCESSIONS A34294; A32892

REFERENCE A34294

#authors Doye, V.; Soubrier, F.; Bauw, G.; Bouterin, M.C.; Beretta, L.; Koppel, J.; Vandekerckhove, J.; Sobel, A.

#journal J. Biol. Chem. (1989) 264:12134-12137

#title A single cDNA encodes two isoforms of stathmin, a developmentally regulated neuron-enriched phosphoprotein.

#cross-references MUID:89308626

#accession A34294

##molecule\_type mRNA

##residues 1-149 ##label DOY

##cross-references GB:J04979

REFERENCE A32892

#authors Schubart, U.K.; Banerjee, M.D.; Eng, J.

#journal DNA (1989) 8:389-398

#title Homology between the cDNAs encoding phosphoprotein p19 and SCG10 reveals a novel mammalian gene family preferentially expressed in developing brain.

#cross-references MUID:89377477

#accession A32892

##molecule\_type mRNA

##residues 1-149 ##label SCH

##cross-references GB:M27876

CLASSIFICATION #superfamily stathmin

SUMMARY #length 149 #molecular-weight 17288 #checksum 2109

Query Match 61.3%; Score 68; DB 5; Length 149;

Best Local Similarity 60.0%; Pred. No. 8.00e-01;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 115 qnaaklerlrekdkh 129

| : : | |||||

Qy 661 QLLSSIEPLREKDKH 675

RESULT 5

ENTRY J01271 #type complete

TITLE hypothetical 21.5K protein - Escherichia coli

ALTERNATE\_NAMES ORFE protein

ORGANISM #formal\_name Escherichia coli

DATE 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 27-Jan-1995

ACCESSIONS J01271; S24198

REFERENCE J01271

#authors Wachi, M.; Doi, M.; Ueda, T.; Ueki, M.; Tsuritani, K.; Nagai, K.; Matsuhashi, M.

#journal Gene (1991) 106:135-136

#title Sequence of the downstream flanking region of the shape-determining genes areBCD of Escherichia coli.

#cross-references MUID:92039056

#accession J01271

##molecule\_type DNA

##residues 1-197 ##label WAC

##cross-references EMBL:X57166

COMMENT The gene encoding for this protein is located at downstream of the are genes.

SUMMARY #length 197 #molecular-weight 21515 #checksum 3123

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 3 17:06:00 1997; MasPar time 9.04 Seconds  
 671.741 Million cell updates/sec

Tabular output not generated.

Title: >US-08-426-509-4  
 Description: (424-659) from US08426509.pep (4 of 5)  
 Perfect Score: 1845  
 Sequence: 1 GSGQFGVVQLGKWKGYDVA.....TIYQIMYSCWHELPEKRPTF 236

Scoring table: PAM 150  
 Gap 11

Searched: 82182 seqs, 25727515 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: pir48  
 1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4  
 8:unann5 9:unann6 10:unann7 11:unann8 12:unann9 13:unenc  
 14:unrev

Statistics: Mean 43.995; Variance 98.402; scale 0.447

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
	1	1327	71.9	659	11	I37212	Bruton agammaglobuli	2.40e-218
	2	1327	71.9	659	11	S28912	protein-tyrosine kin	2.40e-218
	3	1299	70.4	660	12	JN0471	protein-tyrosine kin	4.41e-213
	4	1288	69.8	659	12	B45184	B cell progenitor ki	5.15e-211
	5	1255	68.0	527	12	A55631	protein-tyrosine kin	8.12e-205
	6	1223	66.3	527	4	S13763	protein-tyrosine kin	8.20e-199
	7	1207	65.4	608	4	JU0227	protein-tyrosine kin	8.20e-196
	8	1207	65.4	630	4	JU0228	protein tyrosine kin	8.20e-196
	9	1188	64.4	602	4	JU0215	tyrosine kinase, tec	2.98e-192
	10	1168	63.3	620	4	S33253	protein-tyrosine kin	1.66e-188
	11	1157	62.7	619	4	A47333	T-cell-specific tyro	1.91e-186
	12	1157	62.7	625	4	A43030	protein-tyrosine kin	1.91e-186
	13	1129	61.2	619	4	JN0472	protein-tyrosine kin	3.30e-181
	14	1117	60.5	590	1	TVFFDS	protein-tyrosine kin	5.79e-179
	15	915	49.6	506	4	S24553	protein-tyrosine kin	2.35e-141
	16	860	46.6	362	4	S24551	protein-tyrosine kin	3.54e-131
	17	858	46.5	1520	1	TVFFA	protein-tyrosine kin	8.29e-131
	18	847	45.9	507	4	A39939	protein-tyrosine kin	8.92e-129
	19	844	45.7	505	4	S24550	protein-tyrosine kin	3.19e-128
	20	836	45.3	509	4	A23639	protein-tyrosine kin	9.56e-127
	21	835	45.3	509	1	OKHULK	protein-tyrosine kin	1.46e-126
	22	826	44.8	509	1	TVHAST	protein-tyrosine kin	6.68e-125
	23	824	44.7	308	1	TVFFS	protein-tyrosine kin	1.56e-124

24	823	44.6	542	11	A49114	protein-tyrosine kin	2.39e-124
25	821	44.5	557	10	A00629	protein-tyrosine kin	5.58e-124
26	819	44.4	334	4	S24552	protein-tyrosine kin	1.30e-123
27	820	44.4	697	7	A26132	gag-abl-pol polyprot	8.53e-124
28	817	44.3	1130	1	TVHUA	protein-tyrosine kin	3.05e-123
29	815	44.2	537	4	A43806	protein-tyrosine kin	7.12e-123
30	815	44.2	981	1	F0MVGM	gag-abl polyprotein	7.12e-123
31	815	44.2	1123	4	A39962	kinase-related trans	7.12e-123
32	812	44.0	537	1	TVHUSY	protein-tyrosine kin	2.54e-122
33	809	43.8	505	11	S51647	protein-tyrosine kin	9.07e-122
34	808	43.8	537	1	TVHUSR	protein-tyrosine kin	1.39e-121
35	802	43.5	539	11	B49114	protein-tyrosine kin	1.76e-120
36	800	43.4	536	4	S33569	protein-tyrosine kin	4.12e-120
37	798	43.3	568	1	TVFVS1	protein-tyrosine kin	9.61e-120
38	799	43.3	1146	4	B35962	protein-tyrosine kin	6.29e-120
39	799	43.3	1182	4	A35962	protein-tyrosine kin	6.29e-120
40	797	43.2	526	1	TVFV60	protein-tyrosine kin	1.47e-119
41	797	43.2	532	4	A34104	protein-tyrosine kin	1.47e-119
42	797	43.2	532	4	B34104	protein-tyrosine kin	1.47e-119
43	796	43.1	505	11	I38396	protein-tyrosine kin	2.24e-119
44	796	43.1	541	4	A43610	protein-tyrosine kin	2.24e-119
45	796	43.1	542	1	TVHUSC	protein-tyrosine kin	2.24e-119

# ALIGNMENTS

RESULT 1

ENTRY I37212 #type complete

TITLE Bruton agammaglobulinemia tyrosine kinase - human

ORGANISM #formal\_name Homo sapiens #common\_name man

DATE 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 09-Mar-1996

ACCESSIONS I37212

REFERENCE I37212

#authors Dhta, Y.; Haire, R.N.; Litman, R.T.; Fu, S.M.; Nelson, R.P.; Kratz, J.; Kornfeld, S.J.; de la Morena, M.; Good, R.A.; Litman, G.W.

#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:9062-9066

#title Genomic organization and structure of Bruton agammaglobulinemia tyrosine kinase: localization of mutations associated with varied clinical presentations and course in X chromosome-linked agammaglobulinemia.

#cross-references MUID:94377492

#accession I37212

##status preliminary

##molecule\_type DNA

##residues 1-659 ##label RES

##cross-references ENBL:U10087; NID:g517436; CDS\_PID:g517438

##note only intron-exon junctions are shown

GENETICS

#gene GDB:BTK; AGMX1; IND1

##cross-references GDB:G00-120-542

#map\_position Xq21.33-q22

#introns 47/3; 80/3; 103/3; 131/1; 174/1; 196/3; 259/2; 280/2; 298/3; 325/2; 368/1; 393/1; 450/2; 522/3; 544/2; 584/1; 636/3

SUMMARY #length 659 #molecular-weight 76281 #checksum 9489

Query Match 71.9%; Score 1327; DB 11; Length 659;

Best Local Similarity 67.8%; Pred. No. 2.40e-218;

Matches 160; Conservative 41; Mismatches 35; Indels 0; Gaps 0;

Db 409 gtgqfgvvkygkurgqydvai knikegmsedefieeakvmmnlshelkvlygvctkqr 468

Qy 424 GSG@FGVV@LGKWK@YDVAVKMIKEGMSSEDEFF@EA@TMMKLSHPKLVKFYGVCSKEY 483

Db 469 pifiiteumangcllnulremhrfqtgqllenckdvceaneuleskqflhrdlaarnci 528

```

Qy 484 PIYIVTEYISNGCLLNYLRSHGKGLEPSQLLEMCYDVCEGMAFLESHQFIHRDLAARNCL 543
Db 529 vndqgvvkvdsdflsryvlddeytssvgskfpvrwsppevlmyskfssksdiwafgvlmw 588
|: : |||||:|||||: ||||:||||:||||: | |:||||:||||:|
Qy 544 VDRDLCVKVSDFGMTRYVLDQYVSSVGTKFPVKWSAPEVFHYFKYSSKSDVWAFGILMW 603
Db 589 eiyslgkmpyerftnsetaehiaqglrlyrphlasekvytinyscuhekaderptf 644
|:|||| |: : |: :|| |||||: :| ||||| : : |||
Qy 604 EVFSLGKQPYDLYDNSQVVLKVSQGHRLYRPHLASDTIYQIMYSCWHELPEKRPTF 659

```

RESULT 2

```

ENTRY      S28912      #type complete
TITLE      protein-tyrosine kinase (EC 2.7.1.112) atk - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change
            01-Dec-1995
ACCESSIONS  S28912
REFERENCE   S28912
#authors    Vetrie, D.; Vorechovsky, I.; Sideras, P.; Holland, J.;
            Davies, A.; Flinter, F.; Hammarstrom, L.; Kinnon, C.;
            Levinsky, R.; Bobrow, M.; Smith, C.I.E.; Bentley, D.R.
#journal     Nature (1993) 361:226-233
#title       The gene involved in X-linked agammaglobulinaemia is a member
            of the src family of protein-tyrosine kinases.
#accession   S28912
##status     preliminary
##molecule_type mRNA
##residues    1-659 ##label VET
CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2
            homology
KEYWORDS     phosphotransferase
FEATURE
  221-269     #domain SH3 homology #label SH3\
  281-377     #domain SH2 homology #label SH2\
  400-658     #domain protein kinase homology #label KIN
SUMMARY      #length 659 #molecular-weight 76281 #checksum 9489

```

Query Match 71.9%; Score 1327; DB 11; Length 659;  
 Best Local Similarity 67.8%; Pred. No. 2.40e-218;  
 Matches 160; Conservative 41; Mismatches 35; Indels 0; Gaps 0;

```

Db 409 gtgqfgvvkygkurgqydvaiknikgsnsedefieeakvnmnlshaklvqlygvctkqr 468
|:||||| |||:|||||:|||||:|||||:| ||:| ||| :|||:|:
Qy 424 GSGQFGVVQLGKWKQYDVAVKMIKEGSMSEDEFFQEAQTMMLSHPKLVKFGVCSKEY 483
Db 469 pifiiteymangclllylremhrfqtqqlenckdvceameyleskqflhrdlaarncl 528
|:|:|:|:|:|:|:|:|: :| ||||| ||||:| :|| |:|:|:|:|:|:|
Qy 484 PIYIVTEYISNGCLLNYLRSHGKGLEPSQLLEMCYDVCEGMAFLESHQFIHRDLAARNCL 543
Db 529 vndqgvvkvdsdflsryvlddeytssvgskfpvrwsppevlmyskfssksdiwafgvlmw 588
|: : |||||:|||||:| ||||:||||:||||: | |:||||:||||:|
Qy 544 VDRDLCVKVSDFGMTRYVLDQYVSSVGTKFPVKWSAPEVFHYFKYSSKSDVWAFGILMW 603
Db 589 eiyslgkmpyerftnsetaehiaqglrlyrphlasekvytinyscuhekaderptf 644
|:|||| |: : |: :|| |||||: :| ||||| : : |||
Qy 604 EVFSLGKQPYDLYDNSQVVLKVSQGHRLYRPHLASDTIYQIMYSCWHELPEKRPTF 659

```

RESULT 3

```

ENTRY      JN0471      #type complete
TITLE      protein-tyrosine kinase (EC 2.7.1.112) emb - mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
            12-May-1995

```

ACCESSIONS JN0471  
 REFERENCE JN0471  
 #authors Yamada, N.; Kawakami, Y.; Kimura, H.; Fukamachi, H.; Baier, G.; Altman, A.; Kato, T.; Inagaki, Y.; Kawakami, T.  
 #journal Biochem. Biophys. Res. Commun. (1993) 192:231-240  
 #title Structure and expression of novel protein-tyrosine kinases, Enb and Ent, in the hematopoietic cells.  
 #accession JN0471  
 ##molecule\_type mRNA  
 ##residues 1-660 ##label YAM  
 ##note the nucleotide sequence is not given

# GENETICS

#gene enb  
 CLASSIFICATION #superfamily SH3 homology; protein kinase homology; SH2 homology  
 KEYWORDS phosphotransferase

# FEATURE

223-271 #domain SH3 homology #label SH3\  
 283-379 #domain SH2 homology #label SH2\  
 402-659 #domain protein kinase homology #label KIN\  
 552 #binding\_site phosphate (Tyr) (covalent) #status predicted

SUMMARY #length 660 #molecular-weight 76577 #checksum 1680

Query Match 70.4%; Score 1299; DB 12; Length 660;  
 Best Local Similarity 66.5%; Pred. No. 4.41e-213;  
 Matches 157; Conservative 44; Mismatches 34; Indels 1; Gaps 1;

Db 411 gtgqfgvvkygkurgqydvaikniregsnsedefieeak-vnnlsheklvqlgyvctkqr 469  
 |:||||| |||:|||||||:||||:|||||||:| | :|:| | | | :||||:|:  
 Qy 424 GSGQFGVVQLGKWKQGYDVAVKMIKEGSMSEDEFFQEAQTMKLSHPKLVKFYGVCSKEY 483  
 Db 470 pifiiteymangcllnylrenhrfqtqqlenckdvceameyleskqflhrdlaarncl 529  
 ||:|:||||:||||||| | : ||||| ||||: | || | |:|||||||  
 Qy 484 PIYIVTEYISNGCLLNLYLRSHGKLEPSQLLEMCYDVCEGMAFLESHQFIHRDLAARNCL 543  
 Db 530 vndqgvvksdfglstryvlddeytsvsgskfpvrwspevlmyskfssksdiwafgvlnw 589  
 |: : |||||:|:|||||:| ||||:||||:||||: | |:||||:||||:|  
 Qy 544 VDRDLCVKVSDFGMTRYVLDQYVSSVGTKFPVKWSAPEVFHYFKYSSKSDVWAFGILMW 603  
 Db 590 eiyslgkapyerftnsetaehiaqglrlrphlaservytinyscwhekadepsp 645  
 |:|||| | | : ||: :|| ||||| |||: | ||||| : : ||:  
 Qy 604 EVFSLGKQPYDLYDNSQVVLKVSQGHRLYRPHLASDTIYQINYSCHHELPEKRPTF 659

# RESULT 4

ENTRY B45184 #type complete  
 TITLE B cell progenitor kinase, BPK=cytoplasmic tyrosine kinase - mouse  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 12-May-1995  
 ACCESSIONS B45184  
 REFERENCE A45184  
 #authors Tsukada, S.; Saffran, D.C.; Rawlings, D.J.; Parolini, O.; Allen, R.C.; Klisak, I.; Sparkes, R.S.; Kubagawa, H.; Mohandas, T.; Quan, S.; Belmont, J.W.; Cooper, M.D.; Conley, M.E.; Witte, O.N.  
 #journal Cell (1993) 72:279-290  
 #title Deficient expression of a B cell cytoplasmic tyrosine kinase in human X-linked agammaglobulinemia.  
 #cross-references MUID:93145329  
 #accession B45184  
 ##status preliminary; not compared with conceptual translation  
 ##molecule\_type nucleic acid  
 ##residues 1-659 ##label TSU

```

Db      409 gtgqfgvvkygkurqqydvai kmiregsæsedefieeakvnmnlsheklvqlgygvctkqr 468
      |:||||| |:|:|||||:|:|:|||||:|:|:| |:|:| |:| |:|:|:|:|
Gy      424 GSGQFGVVQLGKWKGGYDVAVKMIKEGSMSEDEFFQEAQTMMKLSHPKLVKFYGVCSKEY 483

Db      469 pifiiteymangcllnlylremhrfqtqqlleackdvceameyleskqflhrdlaarncl 528
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:| |:|:| |:|:| |:|:|:|:|:|
Gy      484 PIYIVTEYISNGCLLNLYLRSHGKGLEPSQLLEMCYDVCEGMAFLESHQFIHRDLAARNCL 543

Db      529 vndqgvvkvslpglsryvlddeytsvsgskfpvrwsppevlmyskfssksdiwafgvlmw 588
      |:|:| |:| |:|:|:|:|:| |:|:|:|:|:|:|:|:| |:|:|:|:|:|:|
Gy      544 VDRDLCVKVSDFGMTRYVLDDQYVSSVGTKFPVKWSAPEVFHYFKYSSKSDVWAFGILMW 603

Db      589 eiyslgkæpyerftnsætaehiaqglrlrphlaservytingyscuhekaderpsf 644
      |:|:|:| |:|:| |:|:|:|:|:|:|:|:|:| |:|:|:|:|:|:|:|:|:|
Gy      604 EVFSLGKQPYDLYDNSQVVVLKVSQGHRLYRPHLASDTIYQIMYSCHWELPEKRPTF 659

```

```

RESULT      5
ENTRY       A55631      #type complete
TITLE       protein-tyrosine kinase (EC 2.7.1.112) rlk - mouse
ALTERNATE_NAMES  resting lymphocyte kinase
ORGANISM     #formal_name Mus sp. #common_name mouse
DATE        23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
              12-May-1995
ACCESSIONS   A55631
REFERENCE    A55631
#authors     Hu, Q.; Davidson, D.; Schwartzberg, P.L.; Macchiarini, F.;
              Lenardo, M.J.; Bluestone, J.A.; Matis, L.A.
#journal      J. Biol. Chem. (1995) 270:1928-1934
#title        Identification of rlk, a novel protein tyrosine kinase with
              predominant expression in the T cell lineage.
#accession    A55631
##status      preliminary
##molecule_type  mRNA
##residues    1-527 ##label HUA
##cross-references  GB:L35268
CLASSIFICATION #superfamily SH3 homology; protein kinase homology
KEYWORDS       phosphotransferase
FEATURE
  89-137        #domain SH3 homology #label SH3\
  269-527        #domain protein kinase homology #label KIN
SUMMARY        #length 527 #molecular-weight 61108 #checksum 785

```

```

Query Match      68.0%; Score 1255; DB 12; Length 527;
Best Local Similarity 65.5%; Pred. No. 8.12e-205;
Matches 156; Conservative 40; Mismatches 38; Indels 4; Gaps 4;

Db      278 gsgqfgvvhlgeurahipvaikainegsmseedfieekvamklshsrllvqlgyvciiqq 337
      |||||::||::|:||||:::|:| ||||:::|:| | |||:
Qu      424 GSGQFGVVVLGKWKQGYDVAVKMIKEGSMSEDEFFQEAQTMMLKSLHPKLVKFYGVCSKEY 483

```

Db 338 plvltfemngclldylrerkqqlkalllsacqdicgmaylerscyihrdlaarnc 396  
 |:|||||:| | | | | : | | : | | | | : | | | | : | | | | |  
 Qy 484 PIYIVTEYISNGCLLNYLRSHGKG-LEPSQLENCYDVCEGMAFLESHQFIHRDLAARNC 542

Db 397 lvssa-cvvkisdfignaryvlddeyisssgakfpvkucppevfhnkyssksdvusfgvl 455  
 | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | |  
 Qy 543 LVDRDLCV-KVSDFGMTRYVLDQYVSSVGTKFPVKWSAPEVFHYFKYSSKSDVWAFGIL 601

Db 456 auevftegapfenksnlqvveaisqgfrlyrphlapntiyrvmyscwhespkgrptf 513  
 | | | | : | | : | | | | : | | | | | : | | | | : | | | | : | | | |  
 Qy 602 MWEVFSLGKQPYDLYDNSQVVLKVSQGHRLYRPHLASDTIYQIMYSCWHELPEKRPTF 659

RESULT 6

ENTRY S13763 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) tec - mouse  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change  
 08-Dec-1995

ACCESSIONS S13763  
 REFERENCE S13763  
 #authors Mano, H.; Ishikawa, F.; Nishida, J.; Hirai, H.; Takaku, F.  
 #journal Oncogene (1990) 5:1781-1786  
 #title A novel protein-tyrosine kinase, tec, is preferentially  
 expressed in liver.  
 #cross-references MUID:91133729  
 #accession S13763  
 ##molecule\_type mRNA  
 ##residues 1-527 ##label MAN  
 ##cross-references EMBL:X55663

GENETICS  
 #gene tec

CLASSIFICATION #superfamily protein-tyrosine kinase src; protein kinase  
 homology; SH2 homology; SH3 homology

KEYWORDS ATP; phosphotransferase; tyrosine-specific protein kinase

FEATURE  
 104-142 #domain SH3 homology #status atypical #label SH3\  
 264-522 #domain protein kinase homology #label KIN

SUMMARY #length 527 #molecular-weight 61556 #checksum 5620

Query Match 66.3%; Score 1223; DB 4; Length 527;  
 Best Local Similarity 61.0%; Pred. No. 8.20e-199;  
 Matches 144; Conservative 45; Mismatches 47; Indels 0; Gaps 0;

Db 273 gsglfgvvrllgkuraqykvaikaireganceedfieekvnmklthpklvqlgyvctqqk 332  
 | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | |  
 Qy 424 GSGQFGVVQLGKWKQGYDVAVKMIKEGSMSEDEFFQEAQTMMLSHPKLVKFYGVCSKEY 483

Db 333 plvltfemngcllnflrqrqghfsrdmllsnqcdvcegmeylernsfihrdlaarnc 392  
 | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | |  
 Qy 484 PIYIVTEYISNGCLLNYLRSHGKGLEPSQLENCYDVCEGMAFLESHQFIHRDLAARNCL 543

Db 393 vneagvvkvsdfgnaryvlddqytsssgakfpvkucppevfnyrsfsksdvusfgvlaw 452  
 | : | | | | | : | | | | | | | : | | | | | : | | | | : | | | | : | | | |  
 Qy 544 VDRDLCVKVSDFGMTRYVLDQYVSSVGTKFPVKWSAPEVFHYFKYSSKSDVWAFGILMW 603

Db 453 eiftegrapfekntngyevvtavtrghrlhrpklatkylgevalrcwqerpegrpsf 508  
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
 Qy 604 EVFSLGKQPYDLYDNSQVVLKVSQGHRLYRPHLASDTIYQIMYSCWHELPEKRPTF 659

RESULT 7

ENTRY JU0227 #type complete  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) tec III - mouse  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 DATE 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change